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/note= "extracellular coding region"
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                                                                                                                                                                                                                             The present sequence represents a human lectin ss3939 polypeptide. The polynuclectide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to identify diseases associated with chromosome 11, as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss3939 gene, and for gene therapy. The ss33939 polypeptides may be useful for developing treatments for diseases (none specified) associated with defective or insufficient amounts of the polypeptides. The antibodies may be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human extracellular matrix and cell adhesion molecule-15 (XMAD-15)
                                                                                                                                  ss1919 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1115; DB 21; Length 374; 100.0%; Pred. No. 3.5e-105; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting the presence of ss3939 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPEETQEEDAKKTFKESREAALNLAY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE03651 standard; Protein; 374 AA.
                                                                                                                                                                                              Claim 12; Page 8; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 206; Conservative
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(IMMV ) IMMUNEX CORP
                                                                          2000-452394/39.
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Best Local Similarity
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                                                                                               N-PSDB; AAA57382
                                     Anderson DA;
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Location/Qualifiers

sapiens.

Homo Key

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The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The copyrucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally letthar gene product and to express a protein which affords protection therapy to correct a genetic deficiency. They are also used for generating casociated with expression of XMAD. They are also used for generating associated with expression of XMAD. They are also used for generating complexes and to create Knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human diseases oligonuclectide or longer caminals (mice or rats) to model human diseases oligonuclectide or longer fragments on a microarray. Antibodies which specifically bind XMAD may be used for the diagnosis of disorders associated with the expression of XMAD, or in assays to monitor patients being treated with XMAD. Diseases adrenoleukodystrophy, solved cell anaemia, thalassaemia, contoince (Aptrophy, sichle cell anaemia, thalassaemia, contoince (Aptrophy, sichle cell anaemia, thalassaemia, contoince (ADDS), Addison's disease, diabetes mellitus, atopic dermatitis, atherosclerosis, Crohn's disease, allergies, anaemia, astomic dermatitis, coereoporosis, psoriasis, rheumatoid arthritis, unital, parasitic, protozoal and helminthic infections and cancer includence and archief warrened and cancer including material and archief and cancer including and archief warrened and cancer including and cancer and archief warrened and cancer including and archief warrened and cancer including and cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human extracellular matrix and cell adhesion molecules and polynuclectide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone marrow, brain and uterus
                                                             "Mature human extracellular matrix and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma
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100.0%; Pred. No. 3.5e-105;
live 0; Mismatches 0;
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Lu DAM, Shah P, Au-Young J;
                                                                                                                           "C-type lectin domain"
                                                                                                                                                                     "C-type lectin domain"
                                                                                                                                                                                                          /note= "Transmembrane motif"
328..348
/note= "Transmembrane motif"
                                                                                   adhesion molecule (XMAD)"
                      'label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0172852.
99US-0172354.
                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-2000; 2000WO-US32990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                WO200142285-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1999;
16-DEC-1999;
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                                         Protein
                                                                                                         Domain
                                                                                                                                                 Domain
                                                                                                                                                                                           Domain
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disorders and platelet disorders such as thrombocytopenia,

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regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and cosquilation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
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                                                                                                               Human; inflammatory condition; shock; sepsis; immune response; cancer: wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyortrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                                                                                                                  CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human novel polymucleotides and associated polypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain issue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                                     61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
               ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEBAKBACRRDGGQLVSIESEDEQKL
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Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                         ABG66680 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human novel polypeptide #15.
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V, Ujwal ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic condition fungal infection
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                                                                                     1 ATGRILSGOPVCRGGTQRPCYKVIYFHDTSRRLWFEEAKEACRRDGGOLVSIESEDEQKL
                                                                                                                   22 ATGRILISGÓPVCRGGTÓRPCYKVIYFHDTSRRINFEEAKEACRRDGGQLVSIESEDEGKL
                                                                                                                                               I EKFI ENLL PSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                            Gaps
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0
                               Length 374;
                                                         0; Indels
                          100.0%; Score 1115; DB 23;
100.0%; Pred. No. 3.5e-105;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 2579.
                                                                                                                                                                                                                                                                                                                                                                         ABB90203 standard; Protein; 374
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                     Query Match
Best Local Similarity 100.
Matches 206; Conservative
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374 AA;
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Sequence
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Whuman; cancer; ulcer; HIV infection; human immunodeficiency virus;
antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antiacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiavascular; antianemic; anaemia;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
w neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
w genetic disease; hematopoietic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; seevee combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                         The invention relates to novel genes (ABL89449-ABL90853) and proteins CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating comedical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's diaease, allorgies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal or when the man are accounted to the man and anoxia anoxia and anoxia and anoxia and anoxia anox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
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Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
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Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AA;
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Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection

Tang YT, Liu C, Drmanac RT

(HYSE-) HYSEQ INC

WPI; 2001-457603/49.

N-PSDB; AAH99737

23-DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317.

22-DEC-2000; 2000WO-US35017

WO200153455-A2 26-JUL-2001. Claim 20; Page 272; 1217pp; English.

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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinifiammatory; antitheumatic; cells they are expressed in, such as: antinifiammatory; antitheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiansent; immunosuppressive; antiadgregant; heamostatic; unlinerary; cardiavascular; antianaemic; antiadgregant; heamostatic; unlinerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; conding them can be used in gene therapy, antidense therapy and vaccine production, The proteins and polynucleotides are useful for screening for conding them can be used in gene therapy, antidense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, thematoid arthritis, septic shock, pancreatitis, cardiac dysfunction, cheumatoid attritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, cardenia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cateoporosis, severe combined immunodeficiency, eczema, allergic rhinitis asthma, diabetes, cancer, multiple sclerosis, depression, chalbeimer's disease, parkinson's disease, neurodegenerative and contrological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
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neurological disorder.

Homo sapiens

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22 ATGRILSGQPVCRGGTQRPCYKVIYFHDTSRRLNPEEAKEACRRDGGQLVSIESEDEQKL

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Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
antiposviatic; cardiant; gene therapy; cancer; neurological disorder;
immune disease; inflammation; blood disorder; tumour.
                  Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
                                                                                                                                                                                                                                   , Florence KA, Youn
Ebner R, Olsen HS,
                                                                                                                                                                                                                                                                                                                      Claim 11; Page 483-484; 634pp; English.
                                                                                                                                                                                                                            Ruben SM,
                                                                                                                                                              98US-0095486.
98US-0095454.
98US-0095455.
                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                        98US-0096319,
                                                                                                                                       99WO-US17130
                                                                                                                                                       98US-0094657
                                                                                                                                                                                                                            Rosen CA,
29-JUN-2000 (first entry)
                                                                                                                                                                                                                          Komatsoulis GA, Rosen CA,
Lafleur D, Wei Y, Ni J,
Soppet DR, Endress GA, E
                                                                                                                                                                                                                                                            WPI; 2000-195282/17.
                                                                                                                                                                                                                                                                     N-PSDB; AAA26385.
                                                                                                     WO200006698-A1.
                                                                                     Homo sapiens.
                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                06-AUG-1998;
12-AUG-1998;
                                                                                                                                                       30-JUL-1998
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The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted conteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAA91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; immunosuppressive; antiHIV; antiHIATMINICATE, inclored; on the corresponding secreted proteins are useful for preventing, treating or antialterpic; osteopathic; antiarthritic; antibacterial; antidabetic; corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the corresponding and proteins are described for each of the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. based on which tissues they are most highly expressed on, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foctal deficiencies, blood disorders, discasses of the immune system, altergies, Alzheimer's and behavioural diseases, inflammation, corresponses, arthritis, infections, AIDS, spinal cord injuries, cardiovascular disorders, reproductive disorders, achievascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polyvucleotides can also be used as food additives or preservatives. Creansplant rejection of the present invention.
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                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Duan R, Moore PA,
, Young PE, Brewer
en HS, Mucenski M;
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Matches 204; Conservative
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CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
             82 IEXFIENLLPSDGDFWIGLRRREEKQSNSTXCQDLYAWTDGSISQFRNWYVDEPSCGSEV
                                                        CVWYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAGGETELTTPV
 61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
                                                                                                                                                                                                                                                   Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvilus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Als; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                      LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                  Amino acid sequence of protein PRO234.
                                                                                                                                                              AAY13367 standard; Protein; 382 AA.
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97US-0059115.
97US-0059117.
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97US-0063541.
97US-0063542.
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97US-0063435.
97US-0063704.
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97US-0063045.
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97US-0063329
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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18-SEP-1997;
15-OCT-1997;
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28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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Query Match

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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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stanabe CK, Wood WI, Zhang Z;
 202 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                                                                                                           Human PRO polypeptide sequence #10.
                                                                                                         AAU29033 standard; Protein; 382
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14-MAR-2000; 2000US-189320P.
15-MAR-2000; 2000US-189320P.
21-MAR-2000; 2000US-190820P.
21-MAR-2000; 2000US-191004P.
21-MAR-2000; 2000US-191040P.
28-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
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2000US-196690P.
2000US-196820P.
2000US-198121P.
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2000US-194449P
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2000US-199397P.
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                                                                                                                                                                         18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-602746/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith V,
                                                                                                                                                                                                                                                                                                                                                                  WO200168848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-2000; 2
06-MAR-2000; 2
14-MAR-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2000;
03-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000;
11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2000;
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25-APR-2000;
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                                                                                                                                         AAU29033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan J,
                                                                                         AAU29033
                                                                       RESULT
                     셤
                                                                                                                           AN13344-403 represent secreted and transmembrane human proteins.

The CDNA sequences are obtained from CDNA libraries, prepared from

CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CT the encoded polypeptides have specific uses based on their homology to

Known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC sasociated with the preservation and maintenance of gastrointestinal

CC uccatated with the preservation and maintenance of gastrointestinal

CC uccatation and congenital maintenance of gastrointestinal

CC uccatation and congenital microvillus arrophy), skin diseases associated

With abnormal keratinocyte differentiation (e.g. psortisms, epithelial

CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),

CC ptent effects on cell growth and development, diseases related to

CC growth or survival of nerve cells including Parkinson's disease,

CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as

CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used

CC Usher Syndrome or Atrophia areata; PRO269 can be used as an

CC uttricrombotic agent; PRO287 Polypeptides and portions may have

CC threapeutic applications in wound healing and tissue repair; PRO317 can

CC be used for treating problems of the kidney, uterus, endometrium, blood

CC vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 BSEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFBEAKEACRRDGGQLVSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and polypeptides used in, e.g. treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                Wood WI, Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 98.7%; Score 1101; DB 20; Best Local Similarity 96.3%; Pred. No. 9.6e-104; Matches 206; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 50; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                Gurney AL,
97US-0063732.
97US-0063734.
97US-0064215.
97US-00642135.
97US-0064103.
97US-0064103.
97US-0064108.
97US-0065186.
97US-0065186.
97US-0065186.
97US-0066120.
97US-0066120.
97US-0066772.
97US-0066772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                              Chen J, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-229533/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX52238
                                29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
                                                                                                                                                                                                                                                                                            24-NOV-1997;
24-NOV-1997;
                                                                                                                      03-NOV-1997
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                                                                                                                                                                        17-NOV-1997
                                                                                                                                                                                                                        21-NOV-1997
                                                                                                                                                        12-NOV-1997
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Gurney AL;

ઠે 유 δ 셤 ò ď ઠે Ä

Goddard ME, Goddard Kljavin IJ; Ferrara N;

L, Eaton DL, H, Gerritsen M Hillan KJ, R Stewart TA,

Tumas D;

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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, theumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                            Desnoyers L,
W, Gerber H,
                                                                                                                                                                                                                                                                                                                                                                             Fong S, Gao W, Gerber H
Grimaldi CJ, Gurney AL,
Pan J, Paoni NF, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 50; 393pp; English
                                                                                   99WO-US20944.
99WO-US21090.
99WO-US21547.
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96.3%;
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      99US-0143048
                                                                                                                                                                       99WO-US28214
                                                                                                                                                                                         99WO-US28313
99WO-US30095
                                                                99WO-US20594
                                                                                                                                                  99WO-US23089
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                                                                                                                                                                                                                                                                                                                                                            Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-081051/09.
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Filvaroff E, Fong &
Godowski PJ, Grimal
Mather JP, Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF72396.
                                                                                   13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams PM,
                                             28-JUL-1999
08-SEP-1999
                                                                                                                                                                                         30-NOV-1999
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ID ABU6
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                                                                                                                                                      Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of fondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also proteins can be used to determine the presence of tumours and also proteins to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian cubjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNWKNNFICKYSDEKPAVPSREAEGE 172
                              presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGRLLS-------GQPVCRGGTQRPCYKVIXFHDTSRRLNFEBAKEACRRDGGQLVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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8
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Pred. No. 9.6e-104;
0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB80235 standard; Protein; 382 AA
                                                                                                                      Claim 11; Fig 20; 774pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.7%;
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Best Local Similarity 96.3
Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 AA;
N-PSDB; AAS45934.
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AAB80235 RESULT

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ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                                                                          1 ATGRLLS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                                                                                     22 ATGRLLSASDLDLRGGOPVCRGGTORPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSI
                                                 Gaps
Score 1101; DB 22; Length 382;
Pred. No. 9.6e-104;
0; Mismatches 0; Indels 8.
                                                                                                                                                                                                                                                                                                                                                                    ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                 ABU69645 standard; Protein; 382 AA.
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Human; secreted and transmembrane protein; gene therapy; psoriasis; enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atheroselerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                         Novel human secreted and transmembrane protein PRO234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US05004.
2000WO-US05841.
2000WO-US07377.
2000WO-US08439.
2000WO-US14042.
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97US-059113P-
97US-059113P-
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97US-059121P-
97US-059121P-
97US-059121P-
97US-059128P-
97US-059268P-
97US-062287P-
97US-062287P-
97US-062281P-
97US-06218P-
97US-06281P-
97US-06218P-
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98WO-US19330.
98WO-US19437.
98WO-US25108.
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99WO-US30095.
99WO-US30911.
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99WO-US28214
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99WO-US28564
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17-0CT-1997
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 97US-063541P.
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97US-063549P.
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WPI; 2003-341586/32.

N-PSDB; ACA54920.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating infilammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 12; Fig 50; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriaais or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for

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2001WO-US1780.
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tumour necrosis factor alpha release, chondrocyte cell; proliferation,
differentiation, tumour; gene therapy.
protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide.
                                                                                                                                                                                                                         ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD
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RR 10-UNN-1998; 98US-061717 P.

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RR 11-UNN-1998; 98US-06172 P.

RR 24-UNN-1998; 98US-06177 P.

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                                                                                                                                    Gaps
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Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
neuroprotective.
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26-AUG-1998,
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Human; secreted protein; transmembrane protein; PRO;
gene therapy; chromosome identification; chromosome marker.
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22-FEB-2000; 2000MO-US03414.
24-FEB-2000; 2000MO-US05004.
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30-MAR-2000; 2000MO-US08439.
22-MAY-2000; 2000MO-US14042.
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Alzheimer's disease or ischaemia, and in various diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy
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Fong S, Gao W, Gerber H, Gerritsen ME, Goddard,
Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Wood WI;
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, 2000WO-US20414.

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                                                                         22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGLVSI
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22-PEB-2000; 2000WO-US05004.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing -
                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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97US - 063734P.
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Query Match

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                                                                    Query Match 98.7%; Score 1101; DB 24; Best Local Similarity 96.3%; Pred. No. 9.6e-104; Matches 206; Conservative 0; Mismatches 0;
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PR 22-JUN-1998; 98US-09165P.
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PR 26-AUG-1998; 98US-09161P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEBAK
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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Q95j96
Q8hyb9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42280 MW; 8AE64E6BC9E56DCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ30977.
Homo sapiens (Human).
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O62623
Q8CJ86
Q8BHK7
Q91ZW4
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Q91ZX0
Q8HY04
Q8SQB2
Q8IXK1
Q9OWI7
Q25459
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Q8BGZ0
Q8CJ94
Q8CJ93
Q8CJ88
Q95LA8
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Q8CJ92
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Q95J96
Q8HYB9
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InterPro, IPR001304; Lectin.C.
Pfam, PP00059; lectin.c; 1.
PROSITE; PS50041; C. TYPE_LECTIN.
Hypothetical protein.
SEQUENCE 374 AA; 42280 MW; 8
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1 MRPGTALQAVLLAVLLVGLR.....PDQMGRSKESGWVENEIYGY 374
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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3: sp_bunan:*
4: sp_tungi:*
5: sp_invertebrate:*
5: sp_mammal:*
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5: sp_mhc:*
6: sp_phage:*
8: p_phage:*
8: p_nage:*
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Gapop 10.0 , Gapext 0.5
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanchori K., Takahashi-Pujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                        DLKNISFRVCSGBATPDDMSCDYDNMAVNPSESGFMTLVSVESGFVTNDIYEFSPDQMGR
DLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EACREDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DGSISGFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPYWFQWNDDRCNMKNNFICKYSD
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

"Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

"R EMBL; AKO55654; BAB70978.1; -.

"R EMBL; AKO55654; Lectin_C;

"R Fam; PRO0039; lectin_c; 1..

"R SMART; SMANC)

"R SMART; EMS0034; CLECT;

"R PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

"R Hypothetical protein.

"SEQUENCE 374 AA; 42310 MW; CBF74E676E23BA16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ31092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%; Score 1996; DB 4;
99.7%; Pred. No. 3.7e-180;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                   374 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.7
Matches 373; Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                        SKESGWVENEIYGY
                                                                                  SKESGWVENEIYGY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomí,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
Strausborg R.;
Strausborg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO25407; AAM25407.1; -.
FinterPro; IPR001304; Lectin_C.
Pfan; PP00059; lectin_c.
Pfan; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to unnamed protein product.
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53 RINFERAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 112
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MEDLINE=22354681; PubMed=1246681;
The FANTOM Consortium Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMEL: AKO86930; BAC39765.1; -.
BMEL: AKO86930; BAC39765.1; -.
SEQÜENCE 211 AA; 23697 MW; AD9870B59E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CS7BL/64; TISSUB=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The FANTOM Consortium of the mouse transcriptome based on functional annotation of 60,770 full-length cONAs.";
Nature 420-563-573 (2002).
EMBL; AK076523; BAC36378.1; -.
SEQUENCE 292 AA; 32502 MW; 73E631C0714D54E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RINFEEAKETCMEDGGQLVSIETEDEQRLIEKFIENLLASDGDFWIGLKRLEEKQSNNTA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.1%; Score 862.5; DB 11; Length 77.7%; Pred. No. 2.6e-73; ive 12; Mismatches 26; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 77.78
Matches 164; Conservative
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        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EACRRDGGQLVSIETEDEGRLIEKFIENLLASDGDFWIGLRRLEVKQVNNTACQDLYAMT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DGSTSQFRNWYVDEPSCGSEVCVVMYHQPSAPPGIGGSYMFQWNDDRCNMKNNFICKYAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BKPA-VPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borowsky M.L., Hynes R.O.;
Borowsky M.L., Hynes R.O.;
Layilin, a novel talin-binding transmembrane protein homologous with
"Layilin, a novel talin-binding transmembrane protein homologous with
"Layilin, a localized in membrane ruffles.";
J. Cell Biol., 143.10.0(1998)
EBMEL, AF093697;
BF093697;
BF0936997;
BF0936997;
BF093697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 VVTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR
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                                                                                                                                                                                                                                                                                                                                                                                   Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TremBlrel. 23, Last annotation update)
LAYILIN homolog (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.9%; Score 1697.5; DB 11; Length 374;
84.7%; Pred. No. 6.2e-152;
ive 23; Mismatches 33; Indels 1;
                                                                                                                                                                                                                       01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                   374 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.7
Matches 316; Conservative
                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cricetulus
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Q8C351;
                                                                                                                                                   Q9Z209
                                                               RESULT 4
Q9Z209
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Q8C351
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1064 QGHCYR--YP---SRRRSWEDAERDCRRRAGHLISIHSQBEHGPINSF-----GHENIW 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMY-HQPSAPA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEOKLIEKFIENLLPSDGDFW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                      Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
"Coordinate Regulation of Cadherin and Integrin Function by the Chondroitin Sulfate Proteoglycan Neurocan.";
Cell Biol. 149:1275-1288 (2000)
EMBL, AFL16856, AAD24546.2;
HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.2%; Score 185; DB 13; Length 12
34.7%; Pred. No. 3.3e-08;
iive 18; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ol-MAR-2003 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Macrophage mannose receptor precursor. MRC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GIGGPYMPQWNDDRCNMKNNFICK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0445; LINK; 2.

PROSITE; PSO0010; ASX HYDROXYL; 1.

PROSITE; PSO00415; C_TYPE_LECTIN_1; 1.

PROSITE; PSO0042; EGF_1; 2.

PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1187; EGF_2; 1.

PROSITE; PSO1187; EGF_2; 1.

PROSITE; PSO1187; EGF_2; 1.
                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig. —
InterPro; IPR00710, Ig.like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR00046; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
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                                                                                                                                                                                  Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR001742; EGF 2.
Interpro; IPR001881; EGF 7.
Interpro; IPR001438; EGF II.
Interpro; IPR001439; EGF II.
                                         WEDLINE=20309833; PubMed=10851024
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Přam; PF00059; lectin_c; 1.
Přam; PF00069; sushi; 1.
Přam; PF00193; Xlink; 1.
PRINTS; PR01265; LINKWODULE.
PRODOM; PD000918; Link; 2.
SMART; SM0013; CCP; 1.
SMART; SM0013; CCP; 1.
SMART; SM0019; EGF_CA; 1.
SMART; SM00199; EGF_CA; 1.
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Best Local Similarity 34.7%,
Local So, Conservative 1
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SEQUENCE 1290
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061830
1D 06188
AC 0618
DT 01-N
DT 01-N
DE MACTY
CS MAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: || || || || || TEPA-----EKPYLTNQ--PEETHENVV-----VTEAGIIPNLIYVIIPTIPLILLILU 233
                                                               127 SQFRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEIHP 186
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                                                                                                                            242 TTVVCWVWICRKRKR-----EQPDPSTKK------QHTIWPSPHQGNSPDL 281
                                                                                                                                                                 234 ALGTCCFOMLHKRKARRHFIKDSTPLSSECLAESLNSNLVHMAGSLIPYHFONNSPSL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE=Forelimb;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
60,770 full-length cDNAs.";
Mature 420:555-573(2002).
EMBL; AROJ1063: BAC27234.1; -.
SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLGAALLCAQGAFARRVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAAL--NLAYILIPSIPLLLLLVV
                                           184 AVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAAL--NLAYILIPSIPLLLLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurocan core protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2010 (Mouse)
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
32.3%; Score 646; DB 11; Length 246;
Best Local Similarity 52.2%; Pred. No. 9.5e-53;
Matches 132; Conservative 34; Mismatches 65; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                         246
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                                                                                                                                                                                                                                                                     PRT;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Q8BMI7
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Q9W6E1
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79 OKLIEKFIENLLPSDGD-FWIGLRR-----REEKQSNSTACQDLYAWTDGSISOFRNWY 131
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MEDLINE=20148849; PubMed=10683150;
MACHINE=20148849; PubMed=10683150;
MACHINE=20148849; PubMed=10683150;
MACHINE=20148849; PubMed=10683150;
MACHINE=20148849; PubMed=1068318; Pubmed=10871200;
MACHINE=108818; Pubmed=10831200;
MACHINE=108818; Pubmed=10831200;
MACHINE=108818; Pubmed=10831200;
MACHINE=108818; Pubmed=1083189;
MACHINE=108818; Pubmed=108818;
MACHINE=108818; Pubmed=1083188;
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MACHINE=108318; Pubmed=108318;
MACHINE=108318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5, Length 1348;
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Last sequence update)
Last annotation update)
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8.9%; Score 177.5; DB 5
Best Local Similarity 28.0%; Pred. No. 1.8e-07;
Matches 47; Conservative 32; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, Endocytic receptor Endol80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              866 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 MFQWNDDRCNMKNNFICK---YSDEKPAVPSREAEGEETELTTPVLPEETQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.9%; Score 178.5; DB 11; Length 1456; Best Local Similarity 25.9%; Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q25199;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NAV-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Tyrosine kinase receptor.
Tyrosine kinase receptor (Hydra vulgaris).
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                        STRAIN=CS7BL/6;
MEDINE=93043353; PubMed=1421407;
Harris N., Rite M., Chang G., Ezekowitz R.B.;
"Characterization of the murine macrophage mannose receptor.";
Blood 80:2363-2373(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR. SEQUENCE 1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Indels
                                                                                                                                                                                                                                                                                  Super M.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97142; Mrc1.
InterPro; IPR000353; AntifreezeII.
InterPro; IPR000363; FN Type II.
InterPro; IPR000372; Ricin_Electin_C.
InterPro; IPR000772; Ricin_Electin_C.
Pfam; PF00040; fn2; I.
Pfam; PF00059; lectin_C.
Pfam; PF00059; Ricin_Blectin; PRINTS; PR00155; ANTIFREEZEII.
PRINTS; PR0013; FNTYPEII; SMATT; SM00059; FNZ; I.
SMATT; SM00059; FNZ; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0615; C_TYPE_LECTIN_1; 6. PROSITE; PSO0041; C_TYPE_LECTIN_2; 8. PROSITE; PSO0023; PIBRONETIN_2; 1. PROSITE; PS50231; RICIN_B_LECTIN; 1.
                                                                                                                                                                                                                                                                                                                               EMBL; Z11974; CAA78028.1; -. HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Conservative
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                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                   SEQUENCE FROM N.A.
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SIGNAL 1
  WCBI_TaxID=10090;
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01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
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MRC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CY ENGUENCE FACUR. N.A.

X TISSUB=Brain;

X MEDLINE=98403880; PubMed=9734811;

X MEDLINE=98403880; PubMed=9734811;

X MEDLINE=98403880; PubMed=9734811;

X Interprove the coding sequences of unidentified human genes. X.

X The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

X The complete sequences of 100 new cDNA clones from brain which can bunk nees. S:169-176(1998).

X The Complete sequences of 100 new cDNA clones from brain which can bunk nees. S:169-176(1998).

X The Complete sequences of 100 new cDNA clones from brain which can bunk nees. S:169-176(1998).

X The Complete sequences of 100 new cDNA clones from brain which can bunk nees. S:169-176(1998).

X The Complete sequences of 100 new cDNA clones from brain which can bunk nees. Since in the complete section.

X The Complete sequences of 100 new cDNA clones from profocode, inform cytrane.

X The Complete sequences of 100 new cDNA clones from profocode, inform cytrane.

X The Complete sequences of 100 new cDNA clones from profocode, inform cytrane.

X The Complete sequences of 100 new cDNA clones from the complete sequences of 100 new cDNA clones.

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X The Complete sequences of 100 new control in the contro
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                                                                                                                                                                                                                                                                                                                          Query Match
8.8%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 2.6e-07;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: | | : : | | 484 IW----GPEG------RWNDSPCNQSLPSICKKAGQLSQGAAREDHG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 192
Prodom; PD000995; FN_Type_II; 1.

SMART; SM00034; CLECT; 8.

SMART; SM00059; RICIN; 1.

SMART; SM00059; RICIN; 1.

PROSITE; PS0041; C_TYPE_LECTIN, 2; 8.

PROSITE; PS00213; FIBRONECTIN, 2; 1.

PROSITE; PS00213; LIPCALIN; 1.

RECEPTOR:

RECEPTO
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RX MEDLINE-9635501; PubMed=8702911;
RA MEDLINE-9635501; PubMed=8702911;
RA WL K., Yuan J., Laaky L.A.;
WL K., Yuan J., Laaky L.A.;
WL K., Yuan J., Laaky L.A.;
RT "Characterization of a novel member of the macrophage mannose receptor type C lectin family.";
Lye C lectin family.";
Lye C lectin family.";
Lye C lectin family.";
Lye C lectin family.";
REMBI: U56734; AAC5729-1;
RICEPPO: IPRO0136; Lactin C.
REMBI: REMBI: U56734; AAC5729-1;
REMBI: REMBI: REMO0136; RICEPPO: REMBI: REMB: REMBI: REMB: REMBI: REMBI: REMBI: REMBI: REMBI: REMBI: REMBI: REMBI: REMB: REMBI: REMB: REMB: REMBI: RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 SGOPVCRGGTORPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIE 87
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1479;
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                                                                                                                                                                                                                                                                                                                                              Query Match 8.8%; Score 176.5; DB 4; Length 1 Best Local Similarity 30.4%; Pred. No. 2.6e-07; Matches 51; Conservative 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                   1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;
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Last sequence update)
Last annotation update)
PROSITE; PS50041; C_TYPE_LECTIN_2; B. PROSITE; PS00023; FIBRONECTIN_2; 1. PROSITE; PS500213; LIPOCALIN; 1. Kinase; Receptor. Kinase; Receptor. SEQUENCE 1479 AA; 166654 MW; C758:
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SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUB=Cerebellum,
MEDLINE=2235468); PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,70 full-length CANAS.";
Nature 420:563-573 (2002).
EMBL; AK082298; BAC38458.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Obtani K., Suzuki Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y.,
Fukuch A., Sakamoto T., Itabe H., Suzutani T., Ogasawara M.,
Yoshida I., Wakamiya N.;
                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chondroitin sulfate proteoglycan 3 (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SEQÜENCE 217 AA; 25949 MW; SF1A6A57B05B76D6 CRC64;
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Last sequence update)
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Q8K4Q8,
01-OCT-2002 (TEMBLEEL 22, C
01-OCT-2002 (TEMBLEEL 22, L
01-MAR-2003 (TEMBLEEL 23, L
Collectin placenta 1.
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SEQUENCE FROM N.A.
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December 22, 2003, 16:05:39; Search time 24.0017 Seconds (without alignments) 2214.797 Million cell updates/sec
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1115
1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_archea:*
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4: Sp_human:*
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7: Sp_mnorebrate:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

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Description	Q8tay8 homo sapien	O92209 cricetulus O8C351 mus musculu	QBDm17 mus musculu QBbvu2 mus musculu Q9w6e1 gallus gall Q61830 mus musculu	Q25199 hydra atten Q9y5p9 homo sapien Q9ubg0 homo sapien O64440 mus	Q8C4f8 mus musculu Q8K4q8 mus musculu Q8C979 mus musculu
RIES					
SUMMARIES	Q8TAY8 Q96NF3	Q92209 Q8C351	Q8BVU2 Q9W6E1 Q61830	Q25199 Q9Y5P9 Q9UBG0 O64449	Q8C4F8 Q8K4Q8 Q8C979
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% Query Match Length DB	374	374 211	246 1290 1456	1348 1479 1479 1479	217 742 742
% Query Match	100.0	72.1	16.0 16.0	15.9 15.8 15.8	14.8 14.8 14.8
Score	1115	945.5 803.5	580 185 178.5	177.5 176.5 176.5	169 165.5 165.5
Result No.	ним	4 ቢ ሊ) L 60 60 ,	10 11 13	14 15 16

ALIGNMENTS

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SUL	AC QBTAY8; DT 01-JUN-2002 (TrEMBLrel. 21, Created)	(TrEMBLrel. 21, Last	DI VI-VOI-ZUUZ (ILEMBLIEL. ZZ, LAST ANNOCATION Update) DE Similar to unnamed protein product.	Homo sapiens (Humar	Eukaryota; Metazoa; Chordata;	OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	RP SEQUENCE FROM N.A.	RC TISSUE=Brain;	Strausberg R.;	RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.		SMART; SM	PROSITE; PS50041	Query Match 100.0%; Score 1115; DB 4; Length 374; Best Local Similarity 100.0%; Drad No. 4 co.00.	6; Conservative 0;	QY 1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL	Db 22 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGLVSIESEDEQKL	QY 61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV	Db 82 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV	Qy 121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAGGETELTTPV	Db 142 CVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV
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RESULT 2 1096NF3 1096NF3 1096NF3 10-01-D
DT 01-D
DT 01-M
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142 CVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IEKFIENLLPSDGDFWIGLRRREEKOSNSTACODLYAWTDGSISOFRNWYVDEPSCGSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzuni Y., Kupimori Y., Komiyama M., Siqiyama T., Irie R., Otsuki T., Sato H., Wakanatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima, A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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85.9%; Pred. No. 9.4e-83;
ive 9; Mismatches 19; Indels 1;
                                                                                                                                                          Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO55654; BAB70978.1;
-InterPro; IRR001304; Lectin.C.
Ffam; PF00059; lectin.c; 1.
SMART; SM00034; CLECT; 1.
Hypothetical protein. C. TYPE_LECTIN.2; 1.
Hypothetical protein.
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HSSP, P22897, 1EGG.
InterPro; IPR001304; Lectin_C.
Pfam; PF000059, Lectin_c. 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 374 AA; 42435 MW; Z98A8BA24FB04E1C CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            Score 1111; DB 4;
Pred. No. 1.1e-98;
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Borowsky M.L., Hynes R.O.;
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RinterPro; IPR001304; Lectin C., RinterPro; IPR001304; Lectin C., Shari PF00059; lectin C.; 1.

SMART; SM00094; CLECT. 1.

R PROSITE; PSS0041: CTYPE_LECTIN_2; 1.

RW Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096NCS;

01-DEC-2001 (TEMBLE1 19, Created)

01-DEC-2001 (TEMBLE1 19, Last sequence update)

01-MAR-2003 (TEMBLE1 23, Last annotation update)

Hypothetical protein FLJ31092.

Hypothetical protein FLJ31092.

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ30977.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LPEETQEEDAKKTFKESREAALNLAY
                                                 202 LPEETQEEDAKKTFKESREAALNLAY
                                                                                                                                                                                PRT;
                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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Gaps

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Length 374; 1; Indels 180 201

62 83

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119 EVCV/MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVPSREAEGEETELT 177
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Forelimb;
MEDLINE=22354683; PubMed=1246681;
The FANTOM Consortium Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cODNs.";
Nature 420:563-573(2002).
EMBL; AK031063; BAC27234.1; -.
SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DECENT TISSUB_AGG TISSUB_Head;

MEDLINE_22354683; PubMed=12466851;

The FANTOM Consortium.

The RAYTOM Consortium.

The RAYTOM Consortium.

The RAYTOM Consortium.

The RAY OF COLD THE MOUSE transcriptome based on functional annotation of 60,770 full-length coNns...;

Mature 420:563-573 (2002).

EMBL; AK076523; BAC36378.1; -.

SEQUENCE 292 AA; 32502 NW; 73E631C0714D54E2 CRC64;
                                                                                                                                                                                                                                                                                                                  23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                                                                          S3 MLQNLTKPGTGISDGDFWIGLLRSGDGQT-SGACPDLYQWSDGSSSGFRNWYTDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                    64 FIENLLP-----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                          4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-type lectin protein MT75 homolog.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.0%; Score 580; DB 11; Length 292; Best Local Similarity 57.9%; Pred. No. 1.1e-47; Matches 110; Conservative 26; Mismatches 40; Indels 14
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 52.0%; Score 580; DB 11; 57.9%; Pred. No. 8.9e-48;
                                                                                                                                                                                                               Query Match 52.0%; Score 580; DB Best Local Similarity 57.9%; Pred. No. 8.9e Matches 110; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBBVU2;
QBBVU2;
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 TPVLPEETQE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO--PEETHE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TPVLPEETQE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
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                                       VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPA-VPSREAEGEETELTTPVL 181
                                                                                                                   KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDEQKLIEKFIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPA-VPSREAEGEE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 GRLLSASDLDPRGGQLVCRGGTRRPCYKVIYFHDAFQRLNFEEAKETCMEDGGQLVSIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAIN=C57BL/64; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
The FANYOM COnsortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analyais of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
NATURE 421: AK086930; BAC39765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-type lectin protein MT75 homolog.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mobil TaxID=10090;

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 AA; 23697 MW; AD9870B5957DD5AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 2.2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
                                                                                                                                                                         PEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                             204 PEETQKEDTKETFKESREAALNLAY 228
                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.1%;
79.8%;
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Q8BMI7,
01-MAR-2003 (TEMBLEEL 23,
01-MAR-2003 (TEMBLEEL 23,
01-MAR-2003 (TEMBLEEL 23,
                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                    LAYILIN homolog (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.8
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELTTPVL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                               123
                                                                                                                                   144
                                                                                                                                                                       182
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ProDom; PD000995; FN TYPE II; 1.
SMART; SM00094; CLBCT; 8
SMART; SM00099; FN2; 1.
SMART; SM00099; RN2; 1.
SMART; SM000498; RICIN; 1.
SMART; SM000498; RICIN; 1.
SMART; SM000498; RICIN; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
PROSITE; PS00023; FIBRONECTIN_2; 8.
PROSITE; PS00023; FIBRONECTIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---WNDINCGYPNNFICORHNSSINATAMP
                                1160 -IG-----KWNDVPCNYNLPYICK 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDAKKTFKESREAALNL 204
   133 GIGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Blood 80:2363-2373 (1992)
                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Super M.;
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Q61830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                                                                                       Neurocan core protein.
Neurocan core protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20309833; PubMed=10851024;

A Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;

T "Coordinate Regulation of Cadherin and Integrin Function by the Chondroitin Sulfate Proteoglycan Neurocan.";

J. Cell Biol. 149:1275-1288 (2000).

R BMBL; AFI16856; AAD24546.2;

R InterPro; IPR00152; ASx hydroxyl.

R InterPro; IPR00152; ASx hydroxyl.

R InterPro; IPR001489; EGF_2.

R InterPro; IPR001489; EGF_1.

R InterPro; IPR001309; Ig_MHC.

R InterPro; IPR0033096; Ig_MHC.

R InterPro; IPR003306; Ig_MHC.

R InterPro; IPR001304; Lectin_C.

R InterPro; IPR000445; Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.6%; Score 185; DB 13; Length 12
Best Local Similarity 34.7%; Pred. No. 7e-09;
Matches 50; Conservative 18; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                             I-NOV-1999 (TrEMBLrel. 12, Created)
I-NOV-1999 (TrEMBLrel. 12, Last sequence update)
I-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                PRT; 1290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
Pfam; PF00047; ig; 1.
Pfam; PF00089; ibctin_c; 1.
Pfam; PF00089; ibctin_c; 1.
Pfam; PF00189; xlink; 2.
PRINTS; PR00010; ibcRinCoD.
PRINTS; PR00010; ibcRinCoD.
PRINTS; PR00010; ibcRinCoD.
PRODOM; PD000918; Link; 2.
SWART; SW00032; CCP; 1.
SWART; SW00034; CCP; 1.
SWART; SW00479; id; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS000186; id; 2.
PROSITE; PS00186; id; 2.
PROSITE; PS01186; id IN; 2.
PROSITE; PS01186; id IN; 2.
PROSITE; PS01186; id IN; 2.
PROSITE; PS01181; id IN; 2.
PROSITE; PS01181; id IN; 2.
                                                                                             PRELIMINARY;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835;
PROSITE; PS01241;
EGF-like domain.
SEQUENCE 1290 A
                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                             09W6E1
09W6E1;
                                                              RESULT
Q9W6E1
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81 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Gaps
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
MEDLINE=9304333; PubMed=1421407;
Harris N., Rits M., Chang G., Ezekowitz R.B.;
"Characterization of the murine macrophage mannose receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

EMBL; 211974; CAA78028.1; -.

HSSP; P22897; 1EGG.

MGD; MGI:97142; MKC1.

InterPro; IPR002353; Antifreezell.

InterPro; IPR00354; Lectin C.

InterPro; IPR00372; Ricin Blectin.

Pfam; PF00040; fn2; 1.

Pfam; PF00059; lectin c; 8.

Pfam; PF00059; Ricin Blectin; 2.

PRINTS; PR000136; ANTIFREEZEII.
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CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
SEQUENCE 1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;
                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage mannose receptor precursor.
PRT; 1456 AA
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67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
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                                                            A Sheikh H., Yarwood H., Ashworth A., Isacke C.;

A sheikh H., Yarwood H., Ashworth A., Isacke C.;

The sheikh H., Yarwood H., Ashworth A., Isacke C.;

The sheigh H., Yarwood H., Ashworth A., Isacke C.;

The sheigh H., Yarwood H., Ashworth A., Isacke C.;

The sheigh H., Ashworth H., Sapressed on fibroblasts, endothelial and macrophages and functions as a lectin receptor.";

The sheigh Aliabase and functions as a lectin receptor.";

The sheigh Aliabase and functions as a lectin receptor.";

The sheigh Aliabase and functions as a lectin receptor.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 176.5; DB 4; Length 30.4%; Pred. No. 5.4e-08; ive 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;
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                                                     MEDLINE=20148849; PubMed=10683150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=98403880; PubMed=9734811;
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Matches 51; Conservative
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                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 ----NRFIENDLIKDNDKYWIGLNKIWNDYLKKNKR-----FEWSDNTYTQFFNWI 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pronom; Prouchs; parimass, 1.

PRINTS; PRO1504; PROCREATITSAP.

PRODOM; PRO0001; Proc. Kinase; 2.

SMART; SM00034; CLECT; 4.

SMART; SM00034; CLECT; 4.

PROSITE; PS00041; C_TYPE_LECTIN 1; 2.

PROSITE; PS50041; C_TYPE_LECTIN 2; 4.

PROSITE; PS50010; PROTEIN KINASE APP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.

SEQUENCE 1348 AA; 156916 MW; 77D2122093227FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Irvine;
MEDLINE=2020940'; PubMed=10744720;
Reidling J.C., Miller M.A., Steele R.E.;
Reidling J.C., Miller Med., Steele R.E.;
Lectin-like Extracellular Domains.";
J. Baol. Chem. 275:10323-10330(2000).
EMBL; L22612; AAA29218.2;
HSSP; P11362; 1FGK.
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Wakaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                           Tyrosine kinase receptor.
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota, Metazoa, Chidaria, Hydrozoa, Hydroida, Anthomedusae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 177.5; DB 5; Length 1348; 28.0%; Pred. No. 3.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 INOPDNNNGIESCVEMNYN------GWSDKECKVLNGFICK 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
955 CFKIFGFANEEKKSWQDARQACKGL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
InterPro; IPR00319; Prot kinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00059; lectin c; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                    Hydridae, Hydra.
NCBI_TaxID=6087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412
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09YSP9
10 09YSP
AC 09YSP
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DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
ON HOMO
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OS EUKAR
OC EUKAR
OC NOBIL
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35; Gaps

Length 1479;

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Dano K.;
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                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dan
"A urokinase receptor-associated protein with specific collagen-
484 IW----GPEG------RWNDSPCNOSLPSICKKAGQLSQGAAEEDHG 520
                                                                                                                                                                                                                                                                                           binding properties.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q8C4F8;
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Q8C4F8
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                                                                                                                                                                                                                                                                                                                                                                               67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=96555501; PubMed=8702911;

Wu K., Yuan J., Lasky L.A.;

"Characterization of a novel member of the macrophage mannose receptor type C lectin family.";

J. Biol. Chem. 271:21323-21330(1996).

EMBL; U56734; AACS2729-1;

HSSP; P02751; 2FR2.
                                                                                                                                                                                                                                                                                                                                 7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                    Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                              124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                            1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  th 15.8%; Score 176.5; DB 4; Similarity 30.4%; Pred. No. 5.4e-08; 51; Conservative 25; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:107818; Mrc2.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001204; Cytochrome P450.
InterPro; IPR001304; Cytochrome P650.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
InterPro; IPR000566; Lipocln cytFABP.
InterPro; IPR000772; Ricin B_lectin.
                                        HSSP, P00751; ZFN2.

InterPro; IPR000562; FN_Type II.

InterPro; IPR001304; Loctin, C.

InterPro; IPR001304; Loctin, C.

InterPro; IPR00072; Ricin, B_lectin. Pfam; PF00040; fn2; I.

ProDom; PF000059; PNTYPEII.

PRODOM; PN00034; CLECT; 8.

SMART; SM000395; FN_TYPE II; I.

SMART; SM00059; FNITYPEII.

PROSITE; PS00615; C_TYPE LECTIN, 1; 3.

PROSITE; PS00615; C_TYPE LECTIN, 1; 3.

PROSITE; PS00613; TIPROMECTIN, 2; 1.

PROSITE; PS00213; FIROMECTIN, 2; 1.

PROSITE; PS00213; FIROMECTIN, 2; 1.

PROSITE; PS00213; FIROMECTIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
for large proteins in vitro.";
es. 5:169-176(1998).
code for large proteins in vit: DNA Res 5:169-176(1998). EMBL; AF107292; ARF14192.1; -- EMBL; AB014609; BAA31684.1; --
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PRINTS; PR00356; ANTIFREEZEII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Pfam; PF00059; lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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MRC2.
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Matches
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Q64449
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384 SWOPF-----OGHCYRL-----OAEKRSWOESKRACLRGGGDLLSIHSMAELEFITKOIK 433
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                                                        54 ERD------FOWTDNTGLQYENWREKOPDNFFAGGEDCVVMVAHESG------R 95
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STRAIN-CSTBL/GG 1 TISSUE=Cerebellum;
STRAIN-CSTBL/GG 1 TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
NATURE 420:563-573 (2002)
NATURE 420:563-573 (2002)
NOW_TER I NOW_TER 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                      'Match 15.2%; Score 169; DB 11; Length 217; Local Similarity 31.1%; Pred. No. 2.9e-08; es 42; Conservative 16; Mismatches 47; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62D456E10B9B48C1 CRC64;
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U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chondroitin sulfate proteoglycan 3 (Fragment).
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Prodom; Prodogs; FN TYPE II; 1.
SWART; SMO0099; FN2; 1.
SWART; SMO0059; FN2; 1.
SWART; SMO0059; FN2; 1.
SWART; SMO0059; FN2; 1.
PROSITE; PSO0086; CYTOCHROME P450; 1.
PROSITE; PSO0041; C_TYPE_LECTIN_1; 3.
PROSITE; PSO0041; C_TYPE_LECTIN_2; 1.
PROSITE; PSO0023; FIBRONECTIN_2; 1.
PROSITE; PSO023; FIBRONECTIN_3; 1.
PROSITE; PSO023; FIBRONECTIN_3; 1.
PROSITE; PSO023; FIBRONECTIN_3; 1.
PROSITE; PSO023; 1.
PROSITE; PSO023; FIBRONECTIN_3; 1
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80 RRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP-SCGSEVCVVMYHQPSAPAGIGGPY 138
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A POLITION K., SUZUKI Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y., Rukuoh A., Sakamoto T., Itabe H., Suzutani T., Ogasawara M., Yoshida I., Wakamoto T., Itabe H., Suzutani T., Ogasawara M., Yoshida I., Wakamoto N.;

T "CDNA cloning of mouse CL-P1 gene.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RMD: ABO78434; BAC05523.1; -.

RMD: MGI:2152907; Colec12.

RMD: MGI:2152907; Colec12.

RICEPPO: IPRO001335; AntifreezeII.

RICEPPO: IPRO01304; Lectin.C.

R FRam; PRO1391; Collagen.

R FRam; PRO0356; ANTIFREEZEII.

R RAMT; SM00034; CLECT; 1.

R RANT; SM00034; CLECT; 1.

R RANT; SM00034; CLECT; 1.

R RANT; CATYPE LECTIN 1; 1.

R ROSITE; PSC0041; CTYPE LECTIN 2; 1.

R ROSITE; PSC0041; CTYPE LECTIN 2; 1.

R ROSITE; PSC0041; CTYPE LECTIN 2; 1.
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                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
COLECI2 OR CL-P1.
COLECI2 OR CL-P1.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; M
      742 AA.
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249..374
/note= "predicted cytoplasmic or intracellular domain"
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/note= "extracellular coding region"
228..248
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ABU71466
ABU71468
ABU65578
ABU65273
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 Amino acid sequenc - App Co-
Human extracellula - Check F
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1 MRPGTALQAVLLAVLLVGLR.......PDQMGRSKESGWVENEIYGY 374
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                            1107863 seqs, 158726573 residues
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                                                                            December 22, 2003, 16:04:13
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Maximum Match 100%
Listing first 45 summaries
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AAE03651
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AAY91490
AAY13367
AAB029033
AABW0235
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                       Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
                                                                                                                     The present sequence represents a human lectin ss1939 polypeptide. The polymorlectide sequence is a source of probes, which may be used to identify nucleic acids encoding ss1939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to identify diseases associated with chromosome 11, as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss1939 gene, and for gene therapy. The ss1939 polypeptides may be useful for developing treatments for amounts of the polypeptides. The antibodies may be useful for developing treatments for detecting the presence of ss1939 polypeptides.
                                                                                                                                                                                                                                                                                                                                                      61 EACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACODLYAWT
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                                                                                                                                                                                                                                                                                           Gaps
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                                                                     883939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
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                                                                                                                                                                                                                                                                    100.0%; Score 2000; DB 21; Length 374; 100.0%; Pred. No. 3.1e-184;
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The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagoinst are used for treating a disease or condition associated or antagoinst are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The polymuclectides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally correct and to express a protein which affords protection associated with expression of XMAD. They are also used for generating chybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic fragments derived from the polynucleotide sequences may be used as clasments on a microarray. Antibodies which specifically bind XMAD may be create from the polynucleotide sequences may be used as clasmosts of disorders associated with XMAD. Diseases clasments on a microarray. Antibodies which specifically bind XMAD may be used for the diagnosis of disorders associated with XMAD. Diseases consective monitor patients being treated with XMAD. Diseases adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's darenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's autenimmune/inflammatory disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, allergies, anaemia, astomic dermatitis, catherosclerosis, Crohn's disease, allergies, anaemia, astomic dermatitis,
                                 Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; crohn's disease; diabetes mellituus; atopic dermatitis; lymphoma; cancer; glomerulomephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic; neuroprotective; dermatological.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mature human extracellular matrix and cell
inflammatory disorder; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;
R, Lu DAM, Shah P, Au-Young J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis, osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal, parasitic, protozoal and helminthic infections and cell proliferative disorders such as actinic keratosis, arteriosclerosis and cancer including breast, bladder, bone marrow, brain and uterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma.
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                                                                                                                                The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB8040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                           Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                     disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAK
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                                                                                                     Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
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Pred. No. 3.1e-184
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Best Local Similarity 100.
Matches 374; Conservative
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N-PSDB; ABL90612
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            antiHiv, antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiatrhritic; antibacterial; antidibbetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
secreted protein; diagnosis; cytostatic; immunosuppressive;
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LA;
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, Young PE, Brewer
                                                                                                                                                                                                                                                                                                                                                                                             , Florence KA, Young PE, Brewe Ebner R, Olsen HS, Mucenski M;
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Pred. No. 2.9e-183
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 483-484; 634pp; English.
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98US-0095486.
98US-0095454.
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98US-0096319.
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Best Local Similarity 99.5
Matches 372, Conservative
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Endress GA,
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                                                                                            VITVVCWVWICKKRKREQPDPSTKKQHIWPSPHQGNSPDLEVYNVIKKSEADLAETRP
                           DGSISQFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSD
                                                                               EKPAVPSREAEGEETELTTPVLPEETQEEDAKKTPKESREAALNLAYILIPSIPLLLLLV
                                                                                                                                    VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRP
                                                                                                                                                                                         DLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gaetrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS, neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
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                                                                                                                                                                                                                                                                                                                                           AAY13367 standard; Protein; 382 AA
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970S-0059263.
970S-0059266.
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17.SEP-1997;
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18.SEP-1997;
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17.OCT-1997;
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24-0CT-1997;
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27-0CT-1997;
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RLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                     CQDLYAWTDGSISQPRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPYMFQWDDRCNMKN
                                                                                                                                    NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS
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                                                                                                                                                                                                                                            ADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYE
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                                                   CODLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMPQWNDDRCNMKN
                                                                                                                  NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS
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      FSPDOMGRSKESGWVENEIYGY 374
                                                                                                                                                                                                                                                                                                                        Human PRO polypeptide sequence #10.
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06. MAR. 2000; 2000US-189320P.
14. MAR. 2000; 2000US-189328P.
15. MAR. 2000; 2000US-189328P.
15. MAR. 2000; 2000US-190828P.
21. MAR. 2000; 2000US-191048P.
21. MAR. 2000; 2000US-191048P.
21. MAR. 2000; 2000US-191048P.
22. MAR. 2000; 2000US-191048P.
23. MAR. 2000; 2000US-193032P.
29. MAR. 2000; 2000US-193032P.
39. MAR. 2000; 2000US-194449P.
11. APR. 2000; 2000US-194449P.
11. APR. 2000; 2000US-19597F.
11. APR. 2000; 2000US-1960P.
11. APR. 2000; 2000US-1961P.
11. APR. 2000; 2000US-1961SP.
25. APR. 2000; 2000US-1981SP.
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2000US-187202P
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The cDNA sequences are obtained from cDNA libraries, prepared from

Cf fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

The encoded polypeptides have specific uses based on their homology to

Known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CK suscoitated with the preservation and maintenance of gastrointestinal

CK concers and the repair of acute and chronic wucosal lesions

CK concers and congenital microvillus atrophy), skin diseases associated

CK with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CK with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CK with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial

CK oncers such as lung squamous cell carcinoma of the vulva and gliomas),

CK of promi effects on cell growth and development, diseases related to

CK of promi effects on cell growth and development, diseases related to

CK of fibromodulin, e.g. for reducing dermal scarring. PRO265 can be used

CK of tibromodulin, e.g. for reducing dermal scarring.

CK of Usher Syndrome or Atrophia areata; PRO533 may be used in the treatment

CK of Usher Syndrome or Atrophia areata; PRO569 can be used as an

CK of Usher Syndrome or Atrophia areata; PRO569 can be used as an

CK of therapeutic agent; PRO287 polypeptides and portions may have

CK of therapeutic applications in wound healing and tissue repair; PRO317 can

CK be used for treating problems of the kidney, uterus, endometrium, blood

CK vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRPGTALQAVLLAVLLVGLRAATGRLLS-----GQPVCRGGTQRPCYKVIYFHDTSR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.3%; Score 1986; DB 20; Length 382;
llarity 97.9%; Pred. No. 7.2e-183;
Conservative 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and polypeptides used in, e.g. gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 50; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard A, Gurney AL,
97US-0063541.
97US-0063542.
97US-0063549.
97US-0063569.
97US-0063564.
97US-0063364.
97US-00637370.
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97US - 0063738
97US - 0064215
97US - 0063735
97US - 0064218
97US - 0064248
97US - 0064248
97US - 0065186
97US - 0065693
97US - 0065693
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97US-0066466.
97US-0066770.
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Best Local Similarity
Matches 374; Conserv
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28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
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31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
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21-NOV-1997;
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24-NOV-1997;
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17-NOV-1997;
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셤
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RLNFEEAKEACRRDGGLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 112

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301 ADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYE 360
                                                                                                                                                                                                                                                                                       antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antianglogenic; vasotropic; antiasthmatic; antiatecr; antiatrhutic; cancer; antiatrhritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
                                                                                                                                                                                                                                                                          dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of sixty one novel secreted and transmembrane RNO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).
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W, Gerber H, Gerritsen
Gurney AL, Hillan KJ,
F, Roy MA, Stewart TA,
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Grimaldi CJ, Gurney AL,
an J, Paoni NF, Roy MA,
Wood WI;
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                                                 FSPDQMGRSKESGWVENEIYGY
                                                                                                                                              AAB80235 standard; Protein; 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US28313.
99WO-US30095.
99WO-US30911.
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99US-0145698
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99WO-US00219,
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                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                       ischaemia; inflammation
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                                                                                                                                                                                                                                         Human PRO234 protein.
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N-PSDB; AAF72396.
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Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                           24-APR-2001
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15-SEP-1999;
05-OCT-1999;
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                                  353
                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumnour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, in mammalian choises. The oligonucleotide probes specific for the PRO nucleic acids subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
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                                                                                                                                                                                                                                                         Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CODLYAWIDGSISOFRNWYVDEPSCGSEVCVVWYHOPSAPAGIGGPYMFQWNDDRCNMKN
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                                                                                                                                                                                                                                                   KP, Chen J, Desnoyers L, Goddard A, Godov
Smith V, Watanabe CK, Wood WI, Zhang Z;
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Pred. No. 7.2e-183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.3%;
                                            22-MAY-2000; 2000MO-US14042.
30-WAY-2000; 2000WO-US14941.
02-UUN-2000; 2000WO-US15264.
05-UUN-2000; 2000US-209812P.
28-JUL-2000; 2000WO-US20710.
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08-NOV-2000; 2000WO-US30952.
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Matches 374; Conservative
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Best Local Similarity
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Pan J,
셤
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Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D;

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970S-059113P
970S-059121P
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970S-063121P.
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97US-059113P.
97US-059115P.
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97US-063435P.
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97US-063544P.
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97US-065186P.
97US-065694P.
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97US-066466P.
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2000WO-US07377
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13-SEP-1999;
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01-DEC-1999;
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05-JAN - 2000;
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24-0CT-1997;
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21-NOV-1997;
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24-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                               1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted and transmembrane protein; gene therapy; psoriasis; entercoolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atheroselscosis; cardiac injury; infertility; birth defect; premature aging; AlDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                                                                                                                                   Gaps
                                                                                                                                                 8
                                                                                                                DB 22; Length 382;
                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein PRO234.
                                                                                                             Query Match 99.3%; Score 1986; DB 22; Best Local Similarity 97.9%; Pred. No. 7.2e-183; Matches 374; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSPDQMGRSKESGWVENEIYGY 374
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98WO-US19177.
98WO-US19330.
98WO-US25108.
99WO-US25108.
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                                                                                382 AA;
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14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
01-DEC-1998;
08-SEP-1999;
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241 IPLLLLLVVTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSE 300
                                                                                                                                                                                                                                                                                                                                           Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood; tumour necrosis factor alpha release; chondrocyte cell; proliferation; differentiation; tumour; gene therapy.
                                                                                                  374
                                                                                                                  361 FSPDQMGRSKESGWVENEIYGY 382
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                                                                                                   PSPDOMGRSKESGWVENE1 YGY
                                                                                                                                                                                                               ABU71121 standard; Protein; 382
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2000WO-US32678.
2000WO-US34956.
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2000WO-US06884.
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2000WO-US14042.
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2000WO-US23328
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2001WO-US17800
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2001WO-US27099.
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97US-063120P.
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                                                                                                                                                                                                                                                                              10-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                              Human PRO234 protein.
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02-MAR-2000;
15-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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02-JUN-2000;
28-JUL-2000;
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01-DEC-2000;
20-DEC-2000;
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01-DEC-1999;
02-DEC-1999;
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22-FEB-2000;
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24-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal culceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriated with abnormal keratinocyte call carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic seril carcinoma, Alzheimer's disease, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, carcaric injury, infertility, birth defects, premature aging, AIDS, cancer, injury, infertility, birth defects, premature aging, AIDS, cancer, also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules or are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQDLYAWTDGSISGFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPYWFQWNDDRCNMKN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                       New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKN
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ME, Goddard A;
Kljavin IJ;
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                                                                                                                                                                                                                                                                                             Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.3%; Score 1986; DB 24; Length 382; 97.9%; Pred. No. 7.2e-183; ive 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                            Eaton DL, F
I, Gerritsen M
Hillan KJ, K
Stewart TA,
                                                                                                                                                                                                                                              Desnoyers L,
W, Gerber H,
                                                                                                                                                                                                                                         Botstein D, Desnoyers L, Fong S, Gao W, Gerber H Grimaldi JC, Gurney AL, an J, Paoni NF, Roy MA,
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97US-069425P.
98US-088026P.
98US-100262P.
98US-100868P.
98US-104080P.
98US-113296P.
99US-113296P.
99US-146698P.
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Matches 374; Conservative
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                                                                                                                                                                                                                                                                                                         Wood WI;
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Filvaroff E, Fong (
Godowski PJ, Grima
Mather JP, Pan J,
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                                               14-SEP-1998;
17-SEP-1998;
13-OCT-1998;
20-NOV-1998;
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PR 22 -CCT -1997; 9718: 0623419
PR 22 -CCT -1997; 9718: 0623419
PR 23 -CCT -1997; 9718: 0623419
PR 24 -CCT -1997; 9718: 0623419
PR 24 -CCT -1997; 9718: 0623419
PR 25 -CCT -1997; 9718: 0623419
PR 25 -CCT -1997; 9718: 0623419
PR 25 -CCT -1997; 9718: 0623419
PR 27 -CCT -1997; 9718: 0663419
PR 11-RE -1997; 9718: 066313
PR 11-RE -1997; 9718: 0663419
PR 11-RE -1998; 9818: 0613419
PR 01-RE -1998; 981
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PR 11—UW-1998 9819-08864P.
PR 11—UW-1998 9819-088661P.
PR 11—UW-1998 9819-089061P.
PR 12—UW-1998 9819-089090P.
PR 12—UW-1998 9819-089514P.
PR 12—UW-1998 9819-089514P.
PR 13—UW-1998 9819-089514P.
PR 13—UW-1998 9819-089514P.
PR 22—UW-1998 9819-089528P.
PR 24—UW-1998 9819-089528P.
PR 24—UW-1998 9819-089528P.
PR 24—UW-1998 9819-089528P.
PR 24—UW-1998 9819-089553P.
PR 24—UW-1998 9819-089553P.
PR 24—UW-1998 9819-089553P.
PR 24—UW-1998 9819-089553P.
PR 25—UW-1998 9819-089553P.
PR 25—UW-1998 9819-089654P.
PR 25—UW-1998 9819-099654P.
PR 17-AUG-1998 9818-09152P.
PR 17-AUG-1998 9818-09152P.
PR 17-AUG-1998 9818-09152P.
PR 17-AUG-1998 9818-09152P.
PR 26—AUG-1998 9818-09152P.
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Ouery Match 99.3%; Score 1986; DB 24; Length 382; Best Local Similarity 97.9%; Pred. No. 7.2e-183; Matches 374; Conservative 0; Mismatches 0; Indels 8

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Gaps

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MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR

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61 RINFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRPGTALQAVLLAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSR
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                18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
21-OCT-1997;
24-OCT-1997;
24-OCT-1997;
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                                                                  CQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPYMFQWNDDRCNWKN 180
                                                                                                                                                                                                             240
                                                                                                              CODLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKN 172
NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS
                                                                                                                                                                                           RINFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted and transmembrane protein; PRO polypeptide; cancer; Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                        361 FSPDQMGRSKESGWVENEIYGY 382
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99WO-US30999.
2000WO-US00219.
2000WO-US03565.
2000WO-US04414.
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98WO-US19330
98WO-US19437
98WO-US25108
99WO-US25084
99WO-US21090
99WO-US21090
99WO-US21090
99WO-US21847.
99WO-US28564.
99WO-US28564.
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2000WO-US23328.
97US-059113P.
97US-059115P.
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16-SEP-1998;
01-DEC-1998;
08-SEP-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
05-OCT-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
03-DEC-1999;
04-DEC-1999;
05-DEC-1999;
06-DEC-1999;
06-DE
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The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences encoding them. The polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating attisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's diseasé or ischaemia, and in various diagnostic assays.

ABU71445-ABU71505 represent human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy
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ME, Goddard P
Kljavin IJ;
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Fong S, Gao W, Gerber H, Gerriteen P
Grimaldi JC, Gurney AL, Hillan KJ, I
an J, Paoni NF, Roy MA, Stewart TA,
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                        9703-059266
9703-062125P.
9703-062287P.
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97US-059117P
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Wood WI;
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Filvaroff E, Fon
Godowski PJ, Gri
Mather JP, Pan J
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Human; secreted protein; transmembrane protein; PRO;
gene therapy; chromosome identification; chromosome marker.
                                                             Human secreted/transmembrane protein PRO234.
               ABU71914 standard; Protein; 382 AA.
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2000WO-USO5004.
2000WO-USO5341.
2000WO-USO7377.
2000WO-USO439.
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05-JAN-2000;
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02-MAR-2000;
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28-JUL-2000;
24-AUG-2000;
                                                                                                    Homo sapiens.
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97US-063329P.
97US-063541P.
97US-063544P.
97US-063549P.
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     28-0CT-1997;
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29-0CT-1997;
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29-0CT-1997;
29-0CT-1997;
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21-0CT-1997;
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21-NOV-1997;
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24-NOV-1997;
24-NOV-1997;
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07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
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(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-329602/31. N-PSDB; ACA60112.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing

Claim 12; Fig 50; 484pp; English.

The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nuclectide sequence encoding one of 6 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CF secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide was recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity) or comparable of sequence encoded by a nucleic acid molecule deposited (b) an amino acid sequence encoded by a nucleic acid molecule deposited (b) an amino acid sequence encoded by a nucleic acid molecule deposited (b) an amino acid sequence encoded by a nucleic acid molecule deposited (b) an isolated signal peptide), a chimaeric molecule comprising a PRO cypeptide of tused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and modulating at least one biological activity of a cell expressing a pro245 or PRO1868 and modulating at least one biological activity of a cell expressing a pro245 or PRO1868 and modulating actids which canimals which may be used in the development and screening of tharapeutically useful reagents. The nucleic acids may be used in cypropetide acids may also be used in tissue typing. Anti-PRO antibodies and nucleic acids may also be used in tissue typing. Anti-PRO antibodies

us-09-887-855-2.rag

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02-DEC-1999; 99WO-US28551.
30-DEC-1999; 09WO-US31274.
05-JAN-2000; 2000WO-US301341.
18-FEB-2000; 2000WO-US04341.
24-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04414.
01-MAR-2000; 2000WO-US05601.
01-MAR-2000; 2000WO-US05841.
01-MAY-2000; 2000WO-US10884.
01-MAY-2000; 2000WO-US14941.
02-JNN-2000; 2000WO-US14941.
03-MAY-2000; 2000WO-US14941.
03-JNN-2000; 2000WO-US14941.
03-JNN-2000; 2000WO-US14941.
03-JNN-2000; 2000WO-US14961.
03-JNN-2000; 2000WO-US30952.
04-NOV-2000; 2000WO-US30952.
05-JUN-2000; 2000WO-US30952.
06-JUN-2000; 2000WO-US30955.
29-JUN-2001; 2001WO-US3166.
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18-SEP-1997,
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18-DEC-1997;
10-MAR-1998;
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     RINFEEAKEACRRDGGLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 112
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                                                                                                                                                                                                                                                                                                              are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents a PRO protein.
                                                                                                                                                              1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR
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                                                                                                                                  8;
                                                                                                Length 382;
                                                                                                                                0; Indels
                                                                                              99.3%; Score 1986; DB 24;
97.9%; Pred. No. 7.2e-183;
tive 0; Mismatches 0;
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98WO-US21141.
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                                                                                           Query Match
Best Local Similarity 97.9<sup>5</sup>
Matches 374, Conservative
                                                                 382 AA
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PR 15-MAY-1998 9 80US 084646P.

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Pred. No. 7.2e-183;
0; Mismatches 0;
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Best Local Similarity 97.9%;
Matches 374; Conservative 0
98US - 096012 P.
98US - 09675 7P.
98US - 09686 7P.
98US - 0968 8 9 P.
98US - 0969 9 P.
98US - 0969 9 P.
98US - 0969 9 P.
98US - 0979 5 P.
98US - 0979 5 P.
98US - 0979 7 P.
98US - 099 10 P.
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98US - 08463P

98US - 08463P

98US - 08657P

98US - 0865P

98US - 0865P

98US - 0881P

98US - 08951B

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98WO-US19330

98WO-US21141

99WO-US25108

99WO-US05028

99WO-US1252

99WO-US1252

99WO-US21012

99WO-US28301

99WO-US28301

99WO-US28301

99WO-US28301

99WO-US28311

2000WO-US05641

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2000WO-US14042

2000WO-US05641

2000WO-US05641

2000WO-US1308

2000WO-US1308
                                                                              2002US-0188769
    US2003036157-A1
                                                                                                                 16-SEP-1998, 07-07-1998, 01-DECT-1998, 08-MAR-1999, 14-MAY-1999, 15-MAR-1999, 15-MAR-1999, 15-MAR-1999, 15-MAR-1999, 15-MAR-1999, 16-MAR-1999, 16-MAR-1999, 16-MAR-2000, 22-FEB-2000, 22-FEB-2000, 22-MAR-2000, 22-MAR-20000, 22-MAR-2000, 22-M
                                                                              02-JUL-2002;
                                       20-FEB-2003
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Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease; postiasis; cancer; lung cancer; colon cancer; nerve cell disease; Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis; atrophia areata; inflammatory disease; asthma; rheumatoid arthritis;
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                                              ABU67368 standard; Protein; 382
                                                                                                                                                                       Human secreted protein PR0234
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98WO-US19177
98WO-US19130
98WO-US194310
98WO-US194310
98WO-US25108
99WO-US25108
99WO-US220854
99WO-US220891
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99WO-US2814
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970S-06344P.
970S-063045P.
970S-063120P.
970S-063121P.
970S-063121P.
970S-063127P.
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Pred. No. 7.2e-183;
); Mismatches 0;
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98US-090662P

98US-091010P

98US-091135P

98US-091135P

98US-0911478P

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es 374; Conserv
  25-JUN-1998, 26-JUN-1998, 26-JUN-1998, 26-JUN-1998, 01-JUL-1998, 01-JUL-1998, 02-JUL-1998, 02-JUL-1998, 02-JUL-1998, 02-JUL-1998, 02-JUL-1998, 03-JUL-1998, 03-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPLILILVVITVVCWVMICKRKREQPDSTKKQHIWPSPHQGNSPDLEVYNVIRKQSE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYE 352
  atrophia areata, angiogenesis, inflammatory disease e.g asthma and rheumatoid arthritis, ischaemia, and in various diagnostic assays. The present sequence represents the amino acid sequence of a PRO polypeptide.
                                                                                                                                                                                                                                                    NFICKYSDEKPAVPSREAEGEETELTTPVLPEETOEEDAKKTFKESREAALNLAYILIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, secreted and transmembrane protein, PRO, TWF-alpha, tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
                                                                                                                                  Query Match 99.3%; Score 1986; DB 24; Length 382; Best Local Similarity 97.9%; Pred. No. 7.2e-183; Matches 374; Conservative 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted/transmembrane protein (PRO) #10.
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99WO-US20111.
99WO-US21090.
99WO-US28301.
99WO-US28551.
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98WO-US25108.
99WO-US05028.
99WO-US10733.
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2000WO-US00219
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                                                                                             382 AA;
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07-OCT-1998;
08-DAR-1999;
08-MAR-1999;
14-MAY-1999;
02-JUN-1999;
15-SEP-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
03-DEC-1999;
05-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease -
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970S - 063327P

970S - 063324P

970S - 063544P

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Filvaroff E, F
Godowski PJ, G
Mather JP, Pan
                       27-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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29-0CT-1997;
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13-OCT-1998;
20-NOV-1998;
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contacting the

proliferation or differentiation of chondrocyte cells by

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18 - FEB - 2000; 2000WO - US04341.
22 - FEB - 2000; 2000WO - US04342.
23 - FEB - 2000; 2000WO - US04444.
24 - FEB - 2000; 2000WO - US05601.
02 - WAR - 2000; 2000WO - US05601.
03 - WAR - 2000; 2000WO - US05611.
15 - WAY - 2000; 2000WO - US05641.
04 - WAY - 2000; 2000WO - US0444.
05 - WAY - 2000; 2000WO - US0444.
05 - WAY - 2000; 2000WO - US0444.
06 - WAY - 2000; 2000WO - US14941.
07 - WAY - 2000; 2000WO - US13494.
08 - JUL - 2000; 2000WO - US13494.
08 - JUL - 2000; 2000WO - US134956.
09 - JUL - 2000; 2000WO - US134956.
09 - JUN - 2001; 2001WO - US134956.
09 - JUN - 2001; 2001WO - US134956.
09 - JUN - 2001; 2001WO - US1369.
09 - JUN - 2001; 2001WO - US1780.
09 - JUN - 2000; 2000WS - OE64510.
09 - MAY - 1999; 99 US - 000WS - OE64510.
09 - MAY - 2001; 2001WS - OE64520.
00 - MAY - 2001; 2001WS - OE65520.
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(GETH) GENENTECH INC.

Gurney AL; Godowski PJ, Goddard A, Gog Desnoyers L, Goauar. רבי רא. Wood WI, Watanabe CK, Chen J, Smith V, Baker KP, Pan J,

WPI; 2003-332039/31. N-PSDB; ACA05709.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification

Claim 11; Fig 20; 706pp; English.

The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the

politication of university and the control of the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the proliferation or differentiation of chondrocytes and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ABU67406-ABU67710 are the PRO polypeptides of the invention. 112 120 180 232 240 292 300 352 CODLYAWIDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMPQWNDDRCNMKN 172 ADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYE 360 25 9 RLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA 61 RLNFEEAKBACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS 241 IPLILLLVYTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSE ADLAETRPDLKNISPRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYE 1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR IPLLLLLLVVTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSE Gaps ., Query Match 99.3%; Score 1986; DB 24; Length 382; Best Local Similarity 97.9%; Pred. No. 7.2e-183; Matches 374; Conservative 0; Mismatches 0; Indels 8 FSPDQMGRSKESGWVENEIYGY 374 382 AA; Sequence 53 113 121 173 233 293 301 353 361 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ 셤 ò 셤 g ò g q ઠ δ ઠે 셤 ò

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Human secreted/tra
Human secreted/tra
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Human pRO polypept
Human secreted/tra
Human secreted/tra
Human pRO polypept
Human pRO1890 poly
Human C-type lecti
Human PRO1890 Ho
Human pRO1890 Ho

secreted/tra secreted/tra human secret

Human Human secreted pro

Human Novel Human Human Human

OM protein

Run on:

Sequence:

Title:

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/note= "predicted cytoplasmic or intracellular domain"
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/note= "signal peptide"
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ABU56273
ABU58409
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ABB84948
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ABU71589
ABU72035
ABU72192
ABU66839
ABU67115
ABU67115
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ABG51278
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Human novel polype
Human polypeptide
Human protein sequ
Human secreted pro
Amino acid sequenc
Human PRO polypept
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(c) 1993 - 2003 Compugen Ltd.
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AAE03651
ABG66680
AAW25796
AAY91490
AAY1367
AAY13367
AAY29033
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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Match Length
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98US-0113820.

23-DEC-1998;

1106 1106 1106 1106 1106 1092 1092

Score

Result Š

Human protein sequ Human liver peptid Protein #3787 enco Peptide #3978 enco Human secreted pro

polypeptide

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Human Novel 1 Human 1

Human Human Human

Novel

angiogenesis PRO1890 prot

Human Human Human

Minimum DB e Maximum DB e

Database

Searched:

Human

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polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative
                                        "Mature human extracellular matrix and cell
                                                                                                                                                                                                                                                                                                                                                                                                               New human extracellular matrix and cell adhesion molecules and
                                                                             /note= "C-type lectin domain"
                                                                                                      "C-type lectin domain"
                                                                                                                                "Transmembrane motif"
                                                                                                                                                            "Transmembrane motif"
                                                                                                                                                                                                                                                                                                                                  l P, Burford N, Azin
Shah P, Au-Young J;
                                                     adhesion molecule (XMAD)"
               'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 108-109; 135pp; English.
                                                                                                                                                                                                                                                                  99US-0172852.
99US-0172354.
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224..247
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fR, Lu DAM,
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                                                                                                                                                                                     WO200142285-A2.
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                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarchoma; inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; atther atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoprosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; arteriosclerosis; noctropic; anticonvulsant; antithyroid; nephrotropic; neuroprotective; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                         present sequence represents a human lectin ss3939 polypeptide. The
                                                                                                                                                                   polynucleotide sequence is a source of probes, which may be used to identify nucleic acids encoding esp393 protefeins, to identify human chromosome number 11, to map genes on human chromosome number 11, to sidentify diseases associated with chromosome 11, as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides may be useful for developing treatments for amounts of the polypeptides. The antibodies may be useful for developing treatments for detecting the presence of ss3939 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                              1 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE
                                                                                                                                                                                                                                                                                                                                                                                                                24 GRILISQQPVCRGGTQRPCYKVIYFHDTSRRINFEEAKBACRRDGGQLVSIESEDEQKLIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                        se3939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
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                                                                                                                                                                                                                                                                                                                                             DB 21; Length 374;
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                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1106; DB 21;
100.0%; Pred. No. 2.5e-104;
tive 0; Mismatches 0;
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                                                                                                                             Claim 12; Page 8; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
(IMMV ) IMMUNEX CORP
                                                WPI; 2000-452394/39.
                                                                                                                                                                                                                                                                                                                  374 AA;
                                                              N-PSDB; AAA57382
                        Anderson DA;
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Patterson C;

Azimzai Y,

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The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagoinst are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The polymuclectides encoding XMAD are useful in somatic or germline gene to therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosi. of disorders associated with expression of XMAD. The maturally occurring genemic sequences and to create knock in humanised animals (pigs) or transgenic hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic continuals (mice or rats) to model human diseases. Oligonuclectide or longer fragments derived from the polymuclectide sequences may be used as elements on a microarray. Antibodies which specifically bind XMAD may be used for the disposses of disorders such as secondars such as acquired immune deficiency cused for the disposses of disorders such as acquired immune deficiency disorders such as acquired immune deficiency syndrome, to bornaria, asthma, asthma, athmas, multiple solerosis, Grave's disease, observative colling, atterioss atherosals, rheumatoid arthritis, ulcerative colling, atterioss atherosals, parasitic, protecal and helminthic infections and cancer including breast, bone matrow, main and natures and cancer including accordance includes actinic main and and anteriors and and cancer including because and cancer including and accordance including and accordance
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Matches 204; Conservative
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disorders and platelet disorders such as thrombocytopenia,

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KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV 120
                                                                                     VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLP 180
                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; fungal infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepais, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                       GRILISGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE
                                                                                                                                                   Liu C, Zhou P, Asundi V, Wang J, Wang D;
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -
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                                                                                                                                                                                                                                                                                                                       ABG66680 standard; Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel polypeptide #15.
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Yamazaki V,
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          regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of steoproration of bone, cartilage, tendon, ligament and/or nerve tissue esteoproratis, bealing of burns, incisions, ulcers, treatment of disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
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100.0%; Pred. No. 2.5e-104;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 204; Conservative
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N-PSDB; ABL90612.
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23-DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317.

(HYSE-) HYSEQ INC

22-DEC-2000; 2000WO-US35017.

WO200153455-A2 26-JUL-2001.

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antiadcerial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
w neuroprotective; antidepressant; nootrophc; antiparkinsonian; infection;
neuroprotective; antidepressant; nootrophc; antiparkinsonian; infection;
munostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
w genetic disease; haematopoletic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
antianaphylactic; parkinson's disease; neurodegenerative disorder;
                                                   The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chamboly autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, theumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1106; DB 23; Length 374;
Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein sequence SEQ ID NO:1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EETQEEDAKKTFKESREAALNLAY 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM25796 standard; Protein; 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 AA;
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ઠે a ઠે 윤 ઠે 셤 ઠ 유 Homo sapiens

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AAM199166 to AAH99904 encode the human proteins given in AAW25225 to
AAW25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinflammatory; antinheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiavascular; antianaemic; antiagregant; hamenostatic; vulnerary;
cardiavascular; antianaemic; antiagregant; hamenostatic; vulnerary;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidation; the proteins and polynucleotides are useful for screening for production; The proteins and polynucleotides are useful for screening for gonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, crheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic disorcers, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, hammandeliciency, eczema, allergic osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, disbetes, cancer, multiple sclerosis, depression, allergic contrological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE 96
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                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1106; DB 22;
100.0%; Pred. No. 2.6e-104;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 272; 1217pp; English.
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                                                                                                                                                                                                                                                                  rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH99737
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24 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNPEBAKEACRRDGGQLVSIESEDEOKLIE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases, heparic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AlbS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are sequences used in the
                                                                               Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiarchma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  χ;
                                        Human secreted protein sequence encoded by gene 40 SEQ ID NO:163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 483-484; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                    98US-0094657.
98US-0095486.
98US-0095454.
98US-0095455.
98US-0096319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                99WO-US17130
29-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                             WO200006698-A1.
                                                                                                                                                                                                                    Homo sapiens.
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06-AUG-1998;
12-AUG-1998;
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61 KPIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV 120
                                           VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLP 180
            84 XFIENLIPSDGDFWIGLRRREEKQSNSTXCQDLYAWTDGSISQFRNWYVDEPSCGSEVCV
                                                      Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psortiasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                                                              Amino acid sequence of protein PRO234.
                                                                                                          227
                                                                                     181 EETQEEDAKKTFKESREAALNLAY 204
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                                                                                                 204 EETQEEDAKKTFKESREAALNLAY
                                                                                                                                                               AAY13367 standard; Protein; 382
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97US-0063327.
97US-0063541.
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97US-0063435.
97US-0063704.
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97US-0063128
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97US-0063544
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97US-0063550
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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28-OCT-1997;
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17-SEP-1997
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18-SEP-1997
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                                                                                                                                         RESULT 7
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99.1%; Score 1096; DB 21; Length 374; 99.0%; Pred. No. 2.6e-103; ive 0; Mismatches 2; Indels 0

Query Match Best Local Similarity 99.03 Matches 202; Conservative

Gaps

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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; deg; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; call proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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Smith V, Watanabe CK, Wood WI, Zhang Z;
  204 ELTIPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                                                                                                                                              Human PRO polypeptide sequence #10.
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                                                                                                                         AAU29033 standard; Protein; 382
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03-MAR-2000; 2000MO-USGS841.
04-MAR-2000; 2000US-185202P.
04-MAR-2000; 2000US-18320P.
14-MAR-2000; 2000US-18320P.
15-MAR-2000; 2000US-193120P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191007P.
22-MAR-2000; 2000US-191032P.
29-MAR-2000; 2000US-191032P.
29-MAR-2000; 2000US-191031-P.
29-MAR-2000; 2000US-191031-P.
29-MAR-2000; 2000US-191031-P.
29-MAR-2000; 2000US-191051-P.
30-MAR-2000; 2000US-191051-P.
31-APR-2000; 2000US-19449P.
31-APR-2000; 2000US-19461P.
31-APR-2000; 2000US-198620P.
31-APR-2000; 2000US-198585P.
35-APR-2000; 2000US-198585P.
35-APR-2000; 2000US-198580P.
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20-DEC-2000; 2000WO-US34956
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                                                                                                                                                                                                       18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                               AAU29033;
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                                                                                                        AAU29033
                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from
fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

The encoded polypeptides have specific uses based on their homology to
known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
associated with the preservation and maintenance of gastrointestinal
mucosa and the repair of acute and chronic mucosal lesions
(e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
mucosa and the repair of acute and chronic mucosal lesions
(e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
mucosa and the repair of acute and chronic mucosal lesions
(c.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
cancers such as lung squamous cell carcinoma of the vulva and gliomas),
concern effects on cell growth and development, diseases related to
growth or survival of nerve cells including Parkinson's disease,
potent effects on cell growth and development, diseases related to
growth or survival of nerve cells including Parkinson's disease,
for fibromodulin, e.g. for reducing dermal scarring. PRO256 can be used
as a target for anti-tumor drugs. PRO331 may be used in the treatment
of Usher Syndrome or Atrophia areata; PRO269 can be used as an
anti-thrombookic agent; PRO287 polypeptides and portions may have
therapeutic applications in wound healing and tissue repair; PRO317 can
be used for treating problems of the kidney, uterus, endometrium, blood
conti-treatment e.g. in the heart of genital tract.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 204
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 50; 320pp; English.
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97US-0063732.
97US-0063734.
97US-0063734.
97US-0064215.
97US-0063175.
97US-0063175.
97US-0065186.
97US-0065186.
97US-0065186.
97US-0065186.
97US-0066120.
97US-0066120.
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Best Local Similarity 96.27
Matches 204; Conservative
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                                       29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
                                                                                                                                        03-NOV-1997;
07-NOV-1997;
12-NOV-1997;
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18-NOV-1997;
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Gurney AL;

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ABU69645 standard; Protein; 382 AA
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                                                                                                       Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of and a control sample of normal cells, whereby a higher level of mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TMF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of fondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also proteins can be used to cervical, or liver tumours, in mammalian character, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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                         Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                             25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiantantation antiantantation; antianglogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthitic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDEOXLIEKFIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP
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                                                                                 Claim 11; Fig 20; 774pp; English.
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Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                       382 AA;
N-PSDB; AAS45934.
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, therosclerosis), inflammatory disorders (e.g. asthma, rheumatorid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as extinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 BDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 SCGSEVCVVWYHQPSAPAGIGGPYMFQWNDDRCNMKQNPICKYSDBKPAVPSREAEGBET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sixty one nucleic acids encoding PRO polypeptides which are useful the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara N;
ME, Goddard A
Kljavin IJ;
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Hillan KJ, H
Stewart TA,
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                                                                                                                                                                                                    99WO-US28214.
99WO-US28313.
99WO-US30095.
                                                                                                                                                                                                                                                                           99WO-US30911.
99WO-US30999.
99WO-US00219.
                                                                                              99WO-US20944.
99WO-US21090.
99WO-US21547.
99US-0143048
                          99US-0145698
99US-0146222
                                                                         99WO-US20594
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N-PSDB; AAF72396.
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Mather JP, Pan J,
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Best Local Similarity
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Filvaroff E,
                                                                 08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
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                                                                                                                                                                                                                            30-NOV-1999
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Human; secreted and transmembrane protein; gene therapy; psoriasis; enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; ALDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                                                                     Novel human secreted and transmembrane protein PRO234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000MO-USO4414.
2000MO-USO5044.
2000MO-USO5041.
2000MO-USO7377.
2000MO-USO3139.
2000MO-US23128.
2000MO-US23128.
2000MO-US23128.
2000MO-US23128.
2000MO-US23128.
97US-059113P.
97US-059113P.
97US-059113P.
97US-05912P.
97US-06312P.
97US-06312P.
97US-06312P.
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98WO-US2108
99WO-US20594
99WO-US21090
99WO-US21090
99WO-US23089
99WO-US2814
99WO-US2814
99WO-US2814
99WO-US2855
99WO-US28565
99WO-US28565
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98WO-US19330
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                                            05-JUN-2003 (first entry)
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13-SEP-1999;
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15-SEP-1999;
16-SEP-1999;
16-SEP-1999;
10-NOV-1999;
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22-MAR-2000;
22-MAR-2000;
23-MAR-2000;
24-MUL-2000;
24-MUL-2000;
24-AUL-2000;
17-SEP-1997;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
                  97US-063541P.
97US-063542P.
97US-063542P.
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29-OCT-1997;
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31-OCT-1997;
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21-NOV-1997;
24-NOV-1997;
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24-NOV-1997;
25-NOV-1997;
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13-OCT-1998;
20-NOV-1998;
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WPI; 2003-341586/32. N-PSDB; ACA54920.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 12; Fig 50; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolities, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for

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02-JUN-2000; 2000WO-US35264.

28-AUG-2000; 2000WO-US320328.

08-NOV-2000; 2000WO-US3128.

08-NOV-2000; 2000WO-US3128.

29-DEC-2000; 2000WO-US3128.

20-DEC-2000; 2000WO-US3126.

20-JUN-2001; 2001WO-US3126.

20-JUN-2001; 2001WO-US3126.

20-JUN-2001; 2001WO-US3126.

20-JUN-2001; 2001WO-US3126.

20-JUN-2001; 2001WO-US3126.

20-JUN-2001; 2001WO-US3136.

21-OCT-1997; 97US-053341P.

28-OCT-1997; 97US-053341P.

29-OCT-1997; 97US-063313P.

21-DEC-1997; 97US-063313P.

21-DEC-1997; 97US-063313P.

21-DEC-1997; 97US-063313P.

21-DEC-1997; 97US-063313P.

21-APR-1998; 98US-077464P.

22-APR-1998; 98US-08139P.

23-APR-1998; 98US-08139P.

23-APR-
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                                                                                                                                                                                                                                                                                               203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
tumour necrosis factor alpha release; chondrocyte cell; proliferation;
differentiation; tumour; gene therapy.
protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for RRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide.
                                                                                                                                               GRLLS--------GQPVCRGGTQRPCYKVIYEHDTSRRLNFEEAKEACRRDGGQLVSIES
                                                                                                                                                                                                        EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP
                                                                                                                                                                                                                        |||||| GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
                                                                                                                            Gaps
                                                                                                                            .
8
                                                                                               24; Length 382;
                                                                                            98.7%; Score 1092; DB 24; Length 96.2%; Pred. No. 7e-103; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     ELTTPVLPEETQEEDAKKTFKESREAALNIAY 204
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99WO-US21030.
99WO-US21031.
99WO-US31274.
99WO-US11274.
2000WO-US00219.
2000WO-US04341.
2000WO-US04341.
2000WO-US04341.
2000WO-US0601.
2000WO-US06841.
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2000WO-US06841.
2000WO-US14042.
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98WO-US21141.
98WO-US25108.
99WO-US10733.
99WO-US1252.
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                                                                                                         Best Local Similarity 96.2
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO234 protein.
                                                                    382 AA;
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07-0CT-1998;
08-MAR-1999;
14-MAY-1999;
02-JUN-1999;
01-SEP-1999;
01-SEP-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
03-DEC-1999;
04-DEC-1999;
05-JAN-2000;
05-JAN-2000;
01-MAR-2000;
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                                                                    Sequence
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                                                                                              Query Match
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EDEOKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 112
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                              Length 382;
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                                                                                                                                                                                                                                           98.7%; Score 1092; DB 24; 96.2%; Pred. No. 7e-103; ive 0; Mismatches 0;
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98US-098014P.
98US-089T3P.
98US-089803P.
98US-09881P.
98US-09863P.
98US-099603P.
98US-099741P.
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2000WO-US00219.
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Best Local Similarity 96.2
Matches 204; Conservative
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14-SEP-1998;
17-SEP-1998;
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13-SEP-1999;
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02-SEP-1998;
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Human; secreted protein; transmembrane protein; PRO; gene therapy; chromosome marker.
                                             Human secreted/transmembrane protein PRO234
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98WO-US19177.
98WO-US19330.
98WO-US19437.
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2000WO-US14042.
2000WO-US15264.
2000WO-US20710.
2000WO-US23328.
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2000WO-US05004
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97US-062816P.
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97US-063128P.
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                   12-JUN-2003 (first entry)
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02-DEC-1999;
16-DEC-1999;
16-DEC-1999;
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24-FEB-2000;
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22-MAY-2000;
28-UUN-2000;
24-AUG-2000;
24-AUG-2000;
                                                                                                                Homo sapiens
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17-SEP-1997;
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27-0CT-1997;
28-0CT-1997;
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17-SEP-1997
       EDEQKLIEKFIENLLPSDGDFWIGLRRREEKOSNSTACQDLYAWTDGSISGFRNWYVDEP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences encoding them. The polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's disease or ischaemia, and in various diagnostic assays.
                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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1 ME, Goddard A;
Kljavin IJ;
Tumas D;
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                                                                                                                                                                                                                   Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, F
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen M
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, K
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI;
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           2000MO-US20710
2000MO-US3328
97US-059113P
97US-059117P
97US-059117P
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N-PSDB; ACA58405.
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22-FEB-2000;
28-AUL-2000;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
16-SEP-1997;
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24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEBAKBACRRDGGQLVSIES 83
                                                             1 GRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
     96.2%; Pred. No. 7e-103;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 6 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CC FRO portein extracellular domain. Also included are a vector comprising the PRO protein extracellular domain. Also included are a vector comprising the PRO protein extracellular cacid, a host cell for the expression of the PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide (having at least 80% sequence identity) or (c) an isolated PRO polypeptide (having at least 80% sequence identity) or (d) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimaeric molecule comprising a PRO containing the polypeptide, a chimaeric molecule comprising a PRO containing the polypeptide, initing a bioactive molecule to a cell expressing a PRO245 or PRO1868 and modulating at least one biological activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used in the development and screening of the propose. The PRO polypeptide are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and concleic acids may also be used in tissue typing. Anti-PRO pulping and in diagnostic asisays for PRO, and in affinity purification of present sequence represents a PRO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Botstein D, Desnoyers L, Eaton DL, Ferrara N;
, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
, Man J, Paoni NF, Roy MA, Stewart TA, Tumas D;
, Wood WI;
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29-OCT-1997; 97US-065435P.
29-OCT-1997; 97US-065734P.
29-OCT-1997; 97US-065734P.
29-OCT-1997; 97US-065734P.
29-OCT-1997; 97US-067738P.
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31-OCT-1997; 97US-06480P.
12-NOV-1997; 97US-065846P.
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17-NOV-1997; 97US-065846P.
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21-NOV-1997; 97US-06653P.
24-NOV-1997; 97US-06646P.
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24-NOV-1997; 97US-06653P.
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N-PSDB; ACA60112.
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Filvaroff E, F
Godowski PJ, C
Mather JP, Par
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98.7%; Score 1092; DB 24; Length 382;

Query Match

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53 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 112
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                                                                                                                                                                                                                 Human; PRO; secreted protein; transmembrane protein; cytostatic; antiarthritic; osteopathic; adrenal tumour; lung troolon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder; cartilage disorder; sports injury.
                                                                                                                                                                                                 Human secreted/transmembrane protein, SEQ ID 20.
                                                                        ELTTPVLPEETQEEDAKKTFKESREAALNLAY 204
                                                                                    204 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 235
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PR 20-DEC-2001 2001MO-U835620.
PR 20-UNN-2001 2001MO-U83166220.
PR 20-UNN-2001 2001MO-U83166220.
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PR 21-CCT-1997 9719 9719 6718262199.
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PR 22-CCT-1997 9719 6718269.
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PR 24-NOV-1997 9719 6719 9718 6719 PR 21-NOV-1997 9719 9719 6719 PR 21-NOV-1997 9719 6719 PR 21-NOV-1997 9719 9719 9719 9719 9719 PR 21-NOV-1997 9719 9719 9719 9719 PR 21-NOV-1997 9719 9719 9719 PR 21-NOV-1997 9719 9719 9719 9719 PR 21-NOV-1997 9719 9719 PR 21-NOV-1997 9719 9719 PR 21-NOV-1997 9719 9719 9719 PR 21-NOV-1997 9719 9719 PR 21-NOV-1997 9719 9719 9719 PR 21-NOV-1997 9719 9719 PR 21-NOV-1997 9719 9719 PR
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                                                                                        GRLLS------GQPVCRGGTQRPCYXVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
                                                                                                     EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP
                                                                                                                                                SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNWKNNFICKYSDEKPAVPSREAEGEET
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; transmembrane protein; cytostatic; gene Therapy; Thr. Agonist-Alpha; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; lever tumour.
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                                           Query Match 98.7%; Score 1092; DB 24; Length 382; Best Local Similarity 96.2%; Pred. No. 7e-103; Matches 204; Conservative 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein PRO234.
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Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

A Geneseq 19Jun03:*

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| SIDS1/gcgdata/geneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqggeneseqgeneseqgeneseqgeneseqgeneseqgeneseqggenes

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	8
Description	Amino acid sequenc Human extracellula Human novel polype Human polypeptide Human protein sequ Human secreted pro Amino acid sequenc Human PRO polypept Human PRO polypept
Ω	AAY93948 AAE03651 ABG66680 ABB90203 AAM25796 AAY91490 AAY13367 AAV13367
DB	222
, Jength	374 374 374 374 382 382
* Query , Match Length DB]	100.0 100.0 100.0 100.0 100.0 98.7
Score	1100 1100 1100 1100 1100 1090 1086 1086
Result No.	

Novel human secret	Human PRO234 prote	Human PRO polypept	Human secreted/tra	Human secreted/tra	Novel human secret	Human secreted pro	Human secreted/tra	Human secreted/tra	Human PRO polypept	Human PRO polypept	Human secreted/tra	Human PRO polypept	Human secreted/tra	Human secreted/tra	A novel polypeptid	Human PRO1890 poly	Human C-type lecti	Human PRO1890. Ho	Human secreted/tra		Human PRO1890 prot		Human PRO polypept	Human secreted pol	Novel human secret	Human PRO polypept	Human PRO polypept		Novel secreted and	Human polypeptide	Human protein segu	Human liver peptid	Protein #3787 enco	Peptide #3978 enco	Human secreted pro
ABU69645	ABU71121	ABU71468	ABU71914	ABU65578	ABU65911	ABU67368	ABU67415	ABU64522	ABU65273	ABU58409	ABU55945	ABU56940	ABU54370	ABU10519	AAB18913	AAU12441	AAB73309	AAB87609	ABG95934	ABB95554	ABB84948	ABU69084	ABU69107	ABU71589	ABU72035	ABU72192	ABU66839	ABU67115	ABU59920	ABP69211	AAB94192	ABG51278	ABB21788	AAM29941	AAY91643
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	21	22	22	22	23	23	23	24	24	24	24	24	24	24	24	53	22	22	22	22	21
382	382	382	382	382	382	382	382	382	382	382	382	382	382	382	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	274	232	102	102	102	81
98.7	98.7	98.7	٠	98.7	98.7	98.7	98.7	98.7																51.0		-	-	•	51.0	•	45.9		٠.		20.5
1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	1086	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	561.5	534.5	504.5	275	275	275	225
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ULT 1 93948 AAY93948 standard; Protein; 374 AA.	AAY93948;	03-OCT-2000 (first entry)	Amino acid sequence of a lectin ss3939 polypeptide.	Human; lectin 883939; chromosome 11; gene therapy.	Homo sapiens.	Kev Location/Onalifiers	tide	Domain 22227	/note= "extracellular coding region" 228 248	Domain 249374	/note= "predicted cytoplasmic or intracellular domain"	WO200039296-A1.	06-JUL-2000.	22-DEC-1999; 99WO-US30523.	23-DEC-1998; 98US-0113820.
SUL Y93	AC AAYS				OS Homo						r. xx			PF 22-D	

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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rhematoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic;
                                                                                                                                                 The present sequence represents a human lectin ss3939 polypeptide. The polymuclectide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 protesins, to identify human chromosome number 11, to map genes on human chromosome number 11, to sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss3339 gene, and for gene therapy. The ss3939 polypeptides may be useful for developing treatments for diseases (none specified) associated with defective or insufficient amounts of the polypeptides. The antibodies may be useful for developing treatments for detecting the presence of ss3939 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                         1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                       25 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPE
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).
                                                                                     ss1939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
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                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1100; DB 21; Length 374; 100.0%; Pred. No. 1e-103; 1ve 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; extracellular matrix and cell adhesion molecule; XMAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE03651 standard; Protein; 374 AA
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                                                                                                                             Claim 12; Page 8; 73pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2001 (first entry)
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Matches 203; Conservative
(IMMV ) IMMUNEX CORP
                                                 2000-452394/39.
                                                                                                                                                                                                                                                                                                             374 AA;
                                                             N-PSDB; AAA57382
                        Anderson DA;
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                                                                                                                                                                                                                                                                                                             Sequence
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Location/Qualifiers

Key

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The present sequence is a human extracellular matrix and cell
adhesion molecule (XMAD). The XMAD is used for screening a compound for
ceffectiveness as an agonist or antagonist of XMAD. The identified agonist
cor antagoinst are used for treating a functional XMAD. The
cor antagoinst are used for treating a functional XMAD. The
cor polynucleotides encoding XMAD are useful in somatic or germline gene
therapy to correct a genetic deficiency, to express a conditionally
clethal gene product and to express a protein which affords protection
against intracellular parasites and also for diagnosis of disorders
associated with expression of XMAD. They are also used for generating
chybridisation probes useful in mapping the naturally occurring genemic
sequences and to create knock in humanised animals (pigs) or transgenic
chybridisation probes useful in mapping the naturally occurring genemic
sequences and to create knock in humanised animals (pigs) or transgenic
chybridisation probes useful in mapping the naturally occurring senomic
sequences and to create knock in humanised animals (pigs) or transgenic
chybridisation probes useful in mapping the naturally bused as
confidents on a microarray. Antibodies which specifically bind XMAD may be
clements on a microarray. Antibodies which specifically bind XMAD. Diseases
considered to reate anoitor patients being treated with XMAD. Diseases
diagnosed, prevented or treated include genetic disorders such as
drenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's
disease, myconic dystrophy, sickle cell anaemia, thalassaemia,
catcolimmune/inflammatory disorders acuch as acquired immune deficiency
syndrome (AIDS), Addison's disease, diaberes mellitus, atopic demantitis,
controlled or preserved diagnosis controlled cysters and an antitis, of the selection of the syndrome deficiency
controlled cysters and controlled cysters and cysters and controlled cysters and cysters 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                  /note= "Mature human extracellular matrix and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patterson C;
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                                                                                                                                                                                                                  'note= "C-type lectin domain"
                                                                                                                                                                                                                                                                                                         "C-type lectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Transmembrane motif"
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AR, Lu DAM, Shah P, Au-Young J;
                                                                                                                                adhesion molecule (XMAD)"
'label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                       /note= "Transmembrane
328..348
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99US-0172354.
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                                                                                                                                                                                                                                                                163..176
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Matches 203; Conservative
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Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sofleroals; cendon; myeloid cell disorder; lymphoid cell disorder; platelat disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion iljury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                                                                                     180
                                                                61 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV 120
                                                                                                                                                       The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                                84
                   85 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV
                                                                                                                                  MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPE
RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
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cell
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RT;
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                                                                                                                                                                                                                                                                                                                      ABG66680 standard; Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel polypeptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2001; 2001WO-US47004.
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7, Ujwal ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection
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Yamazaki V,
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cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthitis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and cosquilation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                 Length 374;
                                                                                                                                                                                                                                                             100.0%; Score 1100; DB 23; Length 100.0%; Pred. No. 1e-103; .ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB90203 standard; Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-2001; 2001WO-US16450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAY-2000; 2000US-205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-122018/16.
                                                                                                                                                                                                                               374 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200190304-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                               Sequence
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WO200153455-A2

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The invention relates to novel genes (ABL89449-ABL50853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating cc medical conditions e.g. by protein or gene therapy. The genes are useful conditional caids, proteins, antibodies and (ant)sponists are useful.

C isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)sponists are useful.

C in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast comparrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune to disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and control procession in the control of prassitic infectious diseases such as viral, bacterial, fungal control of the procession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                         Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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MYHOPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPE 180 61 FIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV 120 85 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV 144 145 MYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPE 204 25 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK . 0 100.0%; Score 1100; DB 23; Length 374; 100.0%; Pred. No. 1e-103; ive 0; Mismatches 0; ETQEEDAKKTFKESREAALNLAY 203 Best Local Similarity 100. Matches 203; Conservative Query Match 181 g ሯ 셤 ठ 셤 ठ

Human protein sequence SEQ ID NO:1311. Ş AAM25796 standard; Protein; 387 (first entry) 16-OCT-2001 AAM25796; RESULT 5

ETQEEDAKKTFKESREAALNLAY 227

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antiniflammatory; antirheumatic; antiarthritic; immunosuppressive; antihiflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cantivasur; antianaemic; anaemia; antihacide; antimutagen; cardiavasular; antianaemic; anaemia; dermatological; antiallergi; antiaschmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; immunostimulant; gene therapy; antiense therapy; vaccine; inflammation; antianaphylactic; rheumatologi arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; cancer; ulcer; HIV infection; human immunodeficiency virus; neurological disorder

Homo sapiens

217

6

Gaps

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AAM99166 to AAH99904 encode the human proteins given in AAW25225 to
AAW25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinflammatory; antinheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiavascular; antianaemic; antiadgaregant; hungicide; antimutagen;
cardiavascular; antianaemic; antiadgaregant; hungicide; antiasthmatic;
antidiabetic; cytostatic; neuroprotective; antidapressant; nootropic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
controparthnoonian; and immunostimulant. The proteins and polymucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polymucleotides are useful for screening for
contropathology, cardiac shork, pancreatitis, cardiac dysfunction,
contropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, hematopoietic disorders,
conteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
chalbeimer's disease, parkinson's disease, neurodegenerative and
contrological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRWWYVDEPSCGSEVCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 MYHQPSAPAGIGGPYMFQWNDDKCNMKNNPICKYSDEKPAVPSKEAEGEETELTTPVLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                      Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1100; DB 22; Length 387; 100.0%; Pred. No. 1.1e-103; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 272; 1217pp; English.
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                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT,
                                                                                                                        23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                              22-DEC-2000; 2000WO-US35017
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Matches 203; Conservative
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                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH99737.
                                       26-JUL-2001.
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N-PSDB; AAA26385.
                                                       Komatsoulis GA,
                         WO200006698-A1.
                     Homo sapiens.
                                  29-JUL-1999;
                                               12-AUG-1998;
                              10-FEB-2000
                                      30-JUL-1998
                                         05-AUG-1998
                                           06-AUG-1998
                                             06-AUG-1998
                                                          Lafleur D,
Soppet DR,
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97US-0062285.
97US-0062287.
97US-0063486.
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97US-0063120.
97US-0063121.
97US-0063127.
97US-0063128.
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97US-0063327.
97US-0063541.
97US-0063542.
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97US-0063549.
97US-0063550.
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97US-0059122
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17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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17-SEP-1997;
17-SEP-1997;
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18-SEP-1997;
18-SEP-1997;
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24-OCT-1997;
24-OCT-1997;
27-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thum becreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; municosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions an be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the polynucleotides. Dased on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, allergies, Alzeimer's and behavioural disorders, schizophrenia, cancer, mannlant such the cancer, in an authrities, infections, AlDS, spinal cord disparsions or present and foetal deficiencies, authrities, infections, AlDS, spinal cord disparsions or present and foetal deficiencies, blood disparsions and foetal deficiencies, blood disparsions and foetal deficiencies, blood disparsions and foetal deficiencies, and behavioural disparse, inflammation, and present deficiencies, blood disparsions and foetal deficiencies, and foetal deficienc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                  Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polynucleotide sequences given in AAA26346 to AAA26458 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels '0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shi Y;
                                                                        Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 99.1%; Score 1090; DB 21; Length 374; Best Local Similarity 99.0%; Pred. No. 1.1e-102; Matches 201; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duan R, Moore PA, Young PE, Brewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GA, Rosen CA, Ruben SM, Duan R, Moore PA, Wei Y, Ni J, Florence KA, Young PE, Brewe Endress GA, Ebner R, Olsen HS, Mucenski M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 483-484; 634pp; English.
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98US-0095454.
98US-0095455.
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29-JUN-2000 (first entry)
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MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPE 180
                                              84
25 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNPEBAKBACRRDGGQLVSIESEDEGKLIEX
                                                                                       145 MYHQPSAPAGIGGPYMFQWNDDRCNMKQNNFICKYSDEKPAVPSREAEGEETELTTPVLPE
                                PIENLL PSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV
                                                                                                                                                                                                                                                                                   Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus arrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Alz; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                                                                                                Amino acid sequence of protein PRO234.
                                                                                                                     181 ETQEEDAKKTFKESREAALNLAY 203
                                                                                                                                 205 ETQEEDAKKTFKESREAALNLAY 227
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                                                                                                                                                                                               AAY13367 standard, Protein; 382
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97US-0063435
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1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 60

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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; deg; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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ith V, Watanabe CK, Wood WI, Zhang Z;
205 LITPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                                                                                                                                                                Human PRO polypeptide sequence #10.
                                                                                                                                 AAU29033 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-196820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198159197P.
25-APR-2000; 2000US-199197P.
25-APR-2000; 2000US-199550P.
25-APR-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US14041.
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22-AUG-2000; 2000WS-0644848.
24-AUG-2000; 2000MO-US23328.
01-DEC-2000; 2000MO-US3952.
01-DEC-2000; 2000MO-US34956.
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05-JUN-2000; 2000US-209832P
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan J,
                                                                                                               AAU2903
                                                                                          RESULT
                                                                                                                                                       The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal lung, fetal factor.

The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal lung, fetal retina.

The encoded polypeptides have specific uses based on their homology to move and the repair of acute and encoded on their homology to associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions of ulceration and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions of ulceration and and congenital microvillus arrophy), skind diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the valva and gliomas), with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the valva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, for fibromodulin, e.g. for reducing dermal scarring. PRO266 can be used as a target for anti-tumor drugs. PRO363 can be used as an a target for anti-tumor drugs. PRO363 can be used as an a target for anti-tumor drugs. PRO363 can be used as an christonestic agent; PRO377 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and polypeptides used in, e.g. treatment
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Pred. No. 2.8e-102;
0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTTPVLPEETQEEDAKKTFKESREAALNLAY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 50; 320pp; English.
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                      970S - 0063738 .
970S - 0064213 .
970S - 0064215 .
970S - 0064215 .
970S - 0064103 .
970S - 0064103 .
970S - 0065186 .
970S - 0066120 .
970S - 0066120 .
970S - 0066120 .
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Best Local Similarity 96.2°
Matches 203, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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                      29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
03-00V-1997;
12-NOV-1997;
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Gurney AL;

Godowski PJ,

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal cand a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be, used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, in mammalian cubjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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                                Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 2.8e-102;
0; Mismatches 0;
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                                                                                                         Claim 11; Fig 20; 774pp; English.
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.2°
Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 AA;
N-PSDB; AAS45934
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CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNWKNNFICKYSDEKPAVPSREAEGEETE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriaais), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, entermial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma. Theumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders usuch as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 DEOKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 RILSASDLDLRGGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE
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illan KJ, Kljavin IJ;
ewart TA, Tumas D;
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Pred. No. 2.8e-102;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 50; 393pp; English.
                                             99WO-US20594.
99WO-US20944.
99WO-US21090.
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99WO-US30911.
99WO-US30999.
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             99US-0145698
99US-0146222
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                                                             13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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204

ABU69645 standard; Protein; 382 AA

RESULT 10 ABU69645

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                                                                                                           Human; secreted and transmembrane protein; gene therapy; psoriasis; enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                                                         Novel human secreted and transmembrane protein PRO234.
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2000WO-US00219
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2000WO-US05841
2000WO-US05842
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24-OCT-1997;
24-OCT-1997;
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27-OCT-1997;
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17-OCT-1997
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97US-063541P.
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98US-113296P.
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12-DEC-1997;
04-JUN-1998;
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28-0CT-1997;
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13-OCT-1998;
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22-DEC-1998;
07-JUL-1999;
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28-JUL-1999
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(GETH) GENENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerriteen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NP, Roy MA, Stewart TA, Tumas D; Wood WI; Pan Williams PM, Ashkenazi A, Filvaroff E, Godowski PJ, Mather JP,

WPI; 2003-341586/32. N-PSDB; ACA54920.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease -

Claim 12; Fig 50; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for

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2000WO-US20710

2000WO-US23328

2000WO-US34956

2000WO-US34956

2001WO-US34956

2001WO-US17600

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2001WO-US21735

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22-JUN-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 28-A-UL-2000) 29-D-UN-2001) 29-D-UN-2001) 29-D-UN-2001) 29-D-UN-2001) 29-D-UN-2001) 29-D-UN-2001) 28-D-UN-2001) 28-
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05-MAY-1998;
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22-MAY-1998;
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29-APR-1998;
29-APR-1998;
29-APR-1998;
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tumour necrosis factor alpha release; chondrocyte cell; proliferation;
differentiation; tumour; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                              CGSEVCVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE
protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide.
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| RLLSASDLDLRGGQPVCRGGTQRPCXKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE
                                                                                                                                                                                                                                                                                                                                                    RLLS------GOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGLVSIESE
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                                                                                                                                                                                                  Gaps
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98WO-US1141.
98WO-US05108.
99WO-US10733.
99WO-US1252.
99WO-US20111.
99WO-US28301.
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2000WO-US0851.
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2000WO-US08541.
2000WO-US08641.
2000WO-US08641.
2000WO-US08414.
2000WO-US08414.
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                                                                                                           382 AA;
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07-OCT 1998;
08-MAR-1998;
08-MAR-1999;
14-MAY 1999;
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|RLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE
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                                                                                                                     Gaps
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Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
neuroprotective.
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                                                                                                   Length 382;
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                                                                                                  Score 1086; DB 24;
Pred. No. 2.8e-102;
0; Mismatches 0;
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98US-098US-098US-98US-098B21P.
98US-098B21P.
98US-098B43P.
98US-099604P.
98US-09961AP.
                                                                                                   tch 98.7%; al Similarity 96.2%; 203; Conservative C
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98WO-US19330.
98WO-US19330.
98WO-US25108.
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99WO-US21090.
99WO-US21090.
99WO-US23089.
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99WO-US28564.
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16-SEP-1998;
17-SEP-1998;
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Human, secreted protein, transmembrane protein, PRO, gene therapy, chromosome identification, chromosome marker.
                                                 Human secreted/transmembrane protein PRO234
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24-FEB-2000; 2000MO-US05004.

02-MAR-2000; 2000MO-US05941.

30-MAR-2000; 2000MO-US05941.

22-MAY-2000; 2000MO-US14042.

02-JUN-2000; 2000MO-US12564.

24-AUG-2000; 2000MO-US12564.

24-AUG-2000; 2000MO-US12564.

24-AUG-2000; 2000MO-US12564.

27-AUG-2000; 2000MO-US12564.
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98WO-US19177.
98WO-US19330.
98WO-US25108.
99WO-US25108.
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97US-062125P.
97US-062287P.
97US-063486P.
97US-063486P.
97US-062814P.
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97US-059117P.
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97US-059184P.
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97US-063120P.
97US-063121P.
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9703-063544P.
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99WO-US21090
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99WO-US30095
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99WO-US28564
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                     12-JUN-2003 (first entry)
                                                                                                                                                US2003003530-A1.
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16-SEP-1998;
01-DEC-1998;
01-DEC-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
03-DEC-1999;
04-DEC-1999;
05-DEC-1999;
06-DEC-1999;
                                                                                                                      Homo sapiens.
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17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
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17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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24-0CT-1997;
27-0CT-1997;
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      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences encoding them. The polynucleotide sequences are useful in molecular biology, as hybridiation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's disease or ischaemia, and in various diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RLLS-----GOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEOKLIEKFIENLLPSDGDFWIGLRRREEKOSNSTACQDLYAWTDGSISQFRNWYVDEPS
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                                                                                                                                                                                                                              , Botstein D, Desnoyers L, Eaton DL, Ferrara N;
, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
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98.7%; Score 1086; DB 24; Length 382;
Best Local Similarity 96.2%; Pred. No. 2.8e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8
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                                                                                                                                                                                                                     Desnoyers L, Ed
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 50; 474pp; English.
2000WO-US0414.
2000WO-US2710.
2000WO-US23128.
97US-059113P.
97US-059117P.
97US-059266P.
97US-062285P.
97US-062287P.
97US-062287P.
97US-062287P.
97US-062287P.
97US-062887P.
97US-062887P.
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Filvaroff E, F
Godowski PJ, C
Mather JP, Par
Williams PM, P
            28-JUL-2000;
24-AUG-2000;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
18-SEP-1997;
17-OCT-1997;
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RESULT 13 ABU71914

Gaps

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53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 112
                                                                                                                                      85 DEQKLIEKPIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 144
                                                                                                                                                                                 113 CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE 172
                                                                                                                                                                                                   145 CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAGGEFF 204
                                                    1 RLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 52
                                                                      cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour; coloh tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder;
                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; secreted protein; transmembrane protein;
      Pred. No. 2.8e-102;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                   205 LTTPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage disorder; sports injury.
                                                                                                                                                                                                                                                                                                                                                                ABU65578 standard; Protein; 382
     96.2%;
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98WO-US25108.
99WO-US05028.
99WO-US10733.
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99WO-US28301
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99WO-US20111
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Matches 203; Conservative
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18-FEB-2000;
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15-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CC for secreted/transmembrane polypeptides, or PRO polypeptide are a vector comprising the PRO protein extracellular domain. Also included are a vector comprising the PRO publypeptide, and recovering the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity) comprising and an amino acid sequence selected from the 61 PRO proteins; comparing an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimaeric molecule comprising a PRO comparing the polypeptide, a chimaeric molecule comprising a PRO containing the polypeptide, inking a bioactive molecule to a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, linking a bioactive molecule to a cell expressing a PRO245 or PRO1868. Nucleic acids which crocde PRO can be used to generate either transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in the development and screening of correcting probes. The PRO polypeptides are useful as molecular markers or in generating probes. The PRO polypeptides are useful as molecular markers or in containing probes. The PRO polypeptides are useful as molecular markers or in generating probes. The PRO polypeptides are useful as molecular markers or in the face acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO. The PRO polypeptides are natural sources. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers L, Eaton DL, Ferrara N; W, Gerber H, Gerritsen ME, Goddard A; Gurney AL, Hillan KJ, Kljavin IJ; NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a PRO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 50; 484pp; English.
97US-063435P.
97US-063704P.
97US-063732P.
97US-063738P.
97US-063738P.
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97US-064248P.
97US-064248P.
97US-064248P.
97US-064248P.
97US-064248P.
97US-066364P.
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Fong S, Gao W,
Grimaldi JC, Gu
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N-PSDB; ACA60112.
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Williams PM,
     29-0CT-1997;
29-0CT-1997;
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29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
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Filvaroff E,
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21-NOV-1997
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2000WO-US32678

01-DEC-2000;

Length 382;

24;

98.7%; Score 1086; DB

Query Match

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PR 20-DEC-2000, 2000W0-U314956.

PR 18-FB2 2001, 2001W0-U514956.

PR 20-UN-2001, 2001W0-U517662.

PR 21-NOV-1997, 97US-06534P.

PR 24-NOCT-1997, 97US-06534P.

PR 24-NOCT-1997, 97US-06534P.

PR 24-NOCT-1997, 97US-065312P.

PR 24-NOCT-1997, 97US-065314P.

PR 24-NR-1998, 98US-0810-98P.

PR 24-NR-1998, 98US-08139P.

PR 24-NR-199
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800 - S08 800 - S08	8US - 088976P 8US - 08912P 8US - 089512P 8US - 089514P 8US - 089514P 8US - 089514P 8US - 089514P 8US - 08952P 8US - 08962P 8US - 090246P 8US - 090444P 8US - 090444P 8US - 090644P 8US - 090640P 8US - 090640P	98US - 090655P. 98US - 090655P. 98US - 090863P. 98US - 091010P. 98US - 091154P. 98US - 091544P. 98US - 091544P. 98US - 091626P. 98US - 091626P. 98US - 091628P. 98US - 091628P. 98US - 091628P. 98US - 091628P. 98US - 095282P. 98US - 095612P. 98US - 095612P. 98US - 096612P. 98US - 096614P. 98US - 097974P. 98US - 096914P.
5 - JUN - 15 5 - JUN - 15 5 - JUN - 15 5 - JUN - 15 6 - JUN - 15 6 - JUN - 15 6 - JUN - 15 6 - JUN - 15 7 - J	2. Jun 199	
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2001MO-US1785.
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03-JUN-1998;
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22-APR-1998;
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29-APR-1998;
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                                                                                            Gaps
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                                                            Length 382;
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                                                         Query Match 98.7%; Score 1086; DB 24; Best Local Similarity 96.2%; Pred. No. 2.8e-102; Matches 203; Conservative 0; Mismatches 0;
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98US-099741P.
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7 note= "extracellular coding region"

228..248

/note= "predicted transmembrane domain"
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/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic;
                                                                                                                                            The present sequence represents a human lectin ss3939 polypeptide. The polymuclectide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to identify diseases associated with chromosome 11, as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides may be useful for developing treatments for amounts of the polypeptides. The antibodies may be useful for developing treatments for detecting the presence of ss3939 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVVMYHQPSAPAGIGGPYMFQWNDBRCNMKNNFICKYSDEKPAVPSREAGGEFELTTPV
                                                                                                                                                                                                                                                                                                                                                                           1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                          61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACODLYAWTDGSISQFRNWYVDEPSCGSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human extracellular matrix and cell adhesion molecule-15 (XMAD-15)
                                                                                    ss1919 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                           DB 21; Length 374;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                         ; Score 1115; DB 21; Pred. No. 3.5e-105, 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE03651 standard; Protein; 374 AA
                                                                                                                       Claim 12; Page 8; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; dermatological
                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 206; Conservative
(IMMV ) IMMUNEX CORP
                                                WPI; 2000-452394/39
                                                                                                                                                                                                                                                                                                  374 AA;
                                                              N-PSDB; AAA57382
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                        Anderson DA;
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                                                                                                                                                                                                                                                                                                   Sequence
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Location/Qualifiers

Key

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The present sequence is a human extracellular matrix and cell
adhesion molecule (XMAD) The XMAD is used for screening a compound for
effectiveness as an agonist or antagonist of XMAD. The identified agonist
or antagoinst are used for treating a disease or condition associated
with decreased or increased expression of functional XMAD. The
conformation of the conformation of functional XMAD. The
polynucleotides encoding XMAD are useful in somatic or germiline gene
therapy to correct a genetic deficiency, to express a conditionally
lethal gene product and to express a protein which affords protection
against intracellular parasites and also for diagnosis of disorders
associated with expression of XMAD. They are also used for generating
hybridisation probes useful in mapping the naturally occurring genomic
consideration probes useful in mapping the naturally occurring genomic
sequences and to create knock in humanised animals (mice or rats) to model human diseases. Oligonuclectic or larangenic
continuals (mice or rats) to model human diseases. Oligonuclectic or larangenic
sequences and correate knock in humanised animals (mice or rats) to model human diseases. Oligonuclectic or larangenic
consideration or ratal concel human diseases. Oligonuclectic or larangenic
consideration of the polynuclectic disorders may be used as
disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
autoimmune/inflammatory disease, alleragies, anaemia, asthma,
contended the contract disease, alleragies, anaemia, asthma,
attended the contract disease, alleragies, anaemia, asthma,
contended the contract or patients and humanic infections and
contential, fungal, parasitic, protozoal and helminthic infections and
cancer including breast, bladder. Den marrow, brain and unerganicallicial protessis and entire warring and entire mice including breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone marrow, brain and uterus
                                                                                                  /note= "Mature human extracellular matrix and cell adhesion molecule (XMAD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and cancer including breast, bladder, bone marrow, brain and utern
cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                            'note= "C-type lectin domain"
                                                                                                                                                                                                                                                                                    'note= "C-type lectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Transmembrane motif"
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Shah P, Au-Young J;
..24
label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                 /note= "Transmembrane
328..348
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99US-0172354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 100.
Matches 206; Conservative
                                                                                                                                                                                                                                                      163..176
                                                                                                                                                                                                                                                                                                                      224 . . 247
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                                                                                                                                                                                  46..63
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16-DEC-1999;
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Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral safetonesis; cendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                                                                 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
                                                                                                                               CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human novel polymucleotides and associated polypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain itssue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
                 1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
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cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid disorders, cancer and promoting wound healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Zhou P,
Drmanac RT;
                                                                                                                                                                                                                  Claim 10; Page 579-580; 672pp; English.
                                                                                                                                                                                                                                                                                                               ABG66680 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel polypeptide #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-2001; 2001WO-US47004.
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Yamazaki V, Ujwal ML,
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N-PSDB; ABK94904.
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regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV
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0
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                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 3.5e-105;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
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                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 206; Conservative
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                                                                                                                                                                                                                                     374 AA;
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                                                                                                                                                                                                                                     Sequence
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WO200153455-A2.

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinator, tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hymonitis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                       Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
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120 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180 201 81 61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 82 IEKFIENLIPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL ö Length 374; 0; Indels DB 23; 100.0%; Score 1115; DB 23; 100.0%; Pred. No. 3.5e-105; 100.0%; Pred. .v. LPEETQEEDAKKTFKESREAALNLAY 206 LPEETOEEDAKKTFKESREAALNLAY 227 Matches 206; Conservative Best Local Similarity 22 121 142 181 Query Match 202 q q g ઠે ò ò

AAM25796 standard; Protein; 387 AA (first entry) 16-OCT-2001 AAM25796; RESULT 5 AAM25796

Human protein sequence SEQ ID NO:1311.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

antinflammatory; antirheumatic; antiarthritic; immunosuppressive;

antinflamcterial; endocrine; cardiant; central nervous system; virucide;

anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eccema;

dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

meuroprofective; antidepressant; nootropic; antiparkinsonian; infection;

meuroprofective; antidepressant; nootropic; antiparkinsonian; infection;

meuroprofective; antidepressant; antiparkinsonian; infection;

meuroprofective; heumatoid arthritis; septic shock; pancreatitis;

cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

mential disease; haematopoietic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

allergic rhinitis; diabetes; multiple sclerosis; depression;

Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; neurological disorder

120

94

180 154

214

sapiens Homo

AAY91490 standard; Protein; 374 AA

AAY91490

AAY91490
ID AAY9
XX
AC AAY9

RESULT 6

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cells they are expressed in such as antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiartlammatory; antirheumatic; central nervous system; virtucide; antiantiantal nervous system; virtucide; antiantense; cardiant; cardiant; antiantamic; antiantamic; antiantamic; antiantamic; antiantense; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidabetic; cytostatic; neuroprotective; antidabetic; screening for antiparxinsonian; and immunostimulant. The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumacoid arthritis, septic shock, pancreatitis, cardiac dysfunction, rheumacoid arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemaia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic thinitis, asthma, diabetes, cancer, multiple sclerosis, depression, antipate and disease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGLVSIESEDEQKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAW25963. The proteins can have activities based on the tissues and
                                                                                                                                                                                                                                                                                                                                                                                                       Isolated human polynuclectides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
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                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT
                                                                                                                                      23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                       22-DEC-2000; 2000WO-US35017.
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                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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us-09-887-855-5.rag

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Human; secreted protein, diagnosis, cytostatic, immunosuppressive, antiHIV, antiinflammatory, nootropic; neuroprotective; antiallergic, osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma, antipostiatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                     Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encoouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                            Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi
Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 483-484; 634pp; English.
                                                                                                                                                                                                    98US-0095486.
98US-0095454.
98US-0095455.
98US-0096319.
                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                       99WO-US17130
                                                                                                                                                                                           98US-0094657
 (first entry)
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                                                                                                                           WO200006698-A1.
                                                                                                        Homo sapiens
 29-JUN-2000
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WO9914328-A2.
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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28-OCT-1997;
28-OCT-1997;
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RESULT 7
AAY13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polynuclectide sequences given in AAA26146 to AAA26458 encode the human secreted proteins given in AAA791451 to AAA791691. The human secreted human secreted proteins given in AAY91451 to AAA791691. The human secreted proteins given in the tissues and cells they are cexpressed in. Examples of the activities are: cytostatic; immunosuppressive; antiHIV; antiHiAlammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidabetic; corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the colymucleotides. Specific uses are described for each of the polymucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foctal deficiencies, blood disorders, discasses of the immune system, allergies, Alzheimer's and behavioural diseases of the immune system, allergies, Alzheimer's and behavioural diseases, inflammation, cortopynasorosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetees, asthma, sepsias, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners.

AAA26337 to AAA26345 and AAY91450 are sequences used in the
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Matches 204, Conservative
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121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                  61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
                                             82 IEXFIENLLPSDGDFWIGLRRREEKQSNSTXCQDLYAWTDGSISQFRNWYVDEPSCGSEV 141
                                                                                        142 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 201
22 ATGRILISGOPVCRGGTORPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEOKL 81
                                                                                                                                                                                                                                                                                    Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                                                                                                                                                                                                                                                        anti-thrombotic, wound healing; tissue repair
                                                                                                                       LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                  Amino acid sequence of protein PRO234.
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                                                                                                                                                                                                AAY13367 standard; Protein; 382
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970S-0062125
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97US - 0059113.
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97US - 0059117.
97US - 0059121.
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Query Match

1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKBACRRDGGQLVSIESEDEQKL 60

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04-APR-2000;
04-APR-2000;
11-APR-2000;
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25-APR-2000;
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03-MAY-2000;
17-MAY-2000;
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                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                     The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal lung, fetal from cDNA libraries, prepared from fetal lung, fetal lung, fetal factor.

The chook sequences are obtained from cDNA libraries, prepared from fetal lung, fetal lung, fetal lung. Fetal retina.

The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chromonic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal uncosa and congenital microvillus arrophy, skind diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), concert effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, ALS, neuropathics or cancer. PRO266 can be used as a target for anti-tumor drugs. PRO369 can be used as an anti-thrombotic agent: PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue specific. PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
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                                                                                                                                                                                                                                                                                                            New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
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8
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Local Similarity 96.3%; Pred. No. 9.6e-104;
les 206; Conservative 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                          Gurney AL, Pennica D, Wood WI,
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                                              97US-0063735.
97US-0063870.
97US-0064103.
             97US-0063738.
97US-0063734.
97US-0064215.
                                                                                                       97US-0065186.
97US-0065846.
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97US-0066120.
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97US-0066466
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                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                          Goddard A,
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24-NOV-1997;
24-NOV-1997;
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            29-0CT-1997;
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29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
01-NOV-1997;
17-NOV-1997;
17-NOV-1997;
17-NOV-1997;
11-NOV-1997;
11-NOV-1997;
11-NOV-1997;
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11-NOV-1997;
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A, God
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desnoyers L, Goduary
                                                                                                                    Human PRO polypeptide sequence #10.
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AAU29033 standard; Protein; 382
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2000US-1930S3P
2000US-1930S3P
2000US-1946439
2000US-194647P
2000US-194647P
2000US-196187P
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2000US-191048P.
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2000US-0644848.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                   WO200168848-A2.
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Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of and a control sample of normal cells, whereby a higher level of an acontrol sample of normal cells, whereby a higher level of an arbbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of fondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also proteins can be used to determine the presence of tumours and also proteins the prostate, rectal, cervical, or liver tumours, in mammalian chasts, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acide can be used for genetic analysis of individuals with genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESEDEOKLIEKFIENLLPSDGDFWIGLRRREEKOSNSTACODLYAWTDGSISQFRNWYVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGRLLS------GOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.7%; Score 1101; DB 22; Length 382; 96.3%; Pred. No. 9.6e-104; ive 0; Mismatches 0; Indels 8
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                                                                                                                                                                                                      Claim 11; Fig 20; 774pp; English
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N-PSDB; AAS45934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptides. The Prosent sections and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin dieeases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthmatheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD
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| ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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                                                                                                                                                                                                                                             Ferrara N;
ME, Goddard A
Kljavin IJ;
                                                                                                                                                                                                                                                                                                                                                                         Sixty one nucleic acids encoding PRO polypeptides which are use the treatment of skin diseases (e.g. psoriasis), cancers (e.g. squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease)
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80
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H, Gerritsen M
Hillan KJ, K
Stewart TA,
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I, Gerber H,
                                                                                                                                                                                                                                          Ashkenazi AJ, Botstein D, Desnoyers L Filvaroff E, Fong S, Gao W, Gerber H Godowski PJ, Grimaldi CJ, Gurney AL, Mather JP, Pan J, Paoni NF, Roy MA, Williams PM, Wood WI,
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          99US-0145698
99US-0146222.
99WO-US20594.
99WO-US21690.
99WO-US21690.
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Matches 206; Conservative
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                                      08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
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20-DEC-1999;
20-DEC-1999;
                                                                                  15-SEP-1999;
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Human; secreted and transmembrane protein; gene therapy; psoriasis, enterocolitis; gastrointestinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; athma; multiple solerosis; organ failure; arthrosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; wound repair; tissue re-growth.
                                                     Novel human secreted and transmembrane protein PRO234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200000-0523318
970S-059113P
970S-059113P
970S-059119P
970S-059121P
970S-059124P
970S-059184P
970S-059268P
970S-059268P
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99WO-US21094
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99WO-US21089
99WO-US28113
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2000WO-US05004.
2000WO-US05841.
2000WO-US07377.
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2000WO-US14042.
2000WO-US15264.
2000WO-US20710.
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2000WO-US03565
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-341586/32. N-PSDB; ACA54920.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease -

Claim 12; Fig 50; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enrearcolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for

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2000WO-UG21328

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2000WO-UG314956

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tumour necrosis factor alpha release; chondrocyte cell; proliferation;
differentiation; tumour; gene therapy.
protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assayys for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human PRO polypeptide.
                                                                                                                                                                                                                                                               ATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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Human; secreted protein; transmembrane protein; PRO;
gene therapy; chromosome identification; chromosome marker.
                                                Human secreted/transmembrane protein PRO234
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2000WO-USOS841
2000WO-USIA4043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences encoding them. The polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or their antibodues are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer, Alzheimer's disease or ischaemia, and in various diagnostic assays.

ABU71445-ABU71505 represent human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy
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 2000WO-US04414.
2000WO-US22710.
2000WO-US2338.
97US-059113P.
97US-059117P.
97US-05926P.
97US-06228FP.
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Best Local Similarity 96.3<sup>5</sup>
Marches 206; Conservative
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N-PSDB; ACA58405.
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22-FEB-2000; 28-JUL-2000; 27-SEP-1997; 17-SEP-1997; 17-SEP-1997; 18-SEP-1997; 15-OCT-1997; 17-OCT-1997; 24-OCT-1997; 24-OCT-1997;
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Pred. No. 9.6e-104;
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22-FEB-2000; 2000MO-US054114.
24-FEB-2000; 2000MO-US05601.
02-MAR-2000; 2000MO-US05601.
15-MAR-2000; 2000MO-US06881.
30-MAR-2000; 2000MO-US06884.
96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or PRO polypeptides or encoding a CT Secreted/transmembrane polypeptides, or PRO polypeptide so a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide (by culturing the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity) comprising a maino acid sequence selected from the 61 PRO proteins; companient and amino acid sequence encoded by a nucleic acid molecule deposited (b) an amino acid sequence encoded by a nucleic acid molecule deposited (with an AFCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimmeric molecule comprising a PRO containing the polypeptide, iniking a bioactive molecule to a cell activity of a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, linking a bioactive molecule to a cell activity of a cell expressing a PRO245 or PRO1868 in a sample suspect of therapeutically useful reagents are useful as an encode markers, or in generating probes. The PRO polypeptica acids may also be used in the development and screening of therapeutically useful reagents. The nucleic acids may be used for protein electrophoresis, and the isolated nucleic acids may be used for protein electrophoresis, and the isolated nucleic acids may be used in tissue typing Anti-PRO polypeptides are useful and in diagnostic assays for PRO. And in a diffinity purification companient cell culture or matural sources. The propersion of protein sequence represents a PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                               Desnoyers L, Eaton DL, Ferrara N; W, Gerber H, Gerritsen ME, Goddard A; Gurney AL, Hillan KJ, Kljavin IJ; NP, ROy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane polypeptides and nucleic acids encoding the
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Fong S, Gao W,
Grimaldi JC, Gur
Pan J, Paoni NF,
                97US-063704P
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Filvaroff E,
Godowski PJ,
Mather JP, Pa
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Query Match

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ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
                                                                                                      EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                                                                                   81
                              22 ATGRILISASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                    1 ATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
Gaps
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                                                                                                                                                                                                                                                                                                             Human; PRO; secreted protein; transmembrane protein; cytostatic; antiarthritic; osteopathic; adrenal tumour; lung troolon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; TNP-alpha release; arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder; cartilage disorder; sports injury.
0; Indels
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                                                                                                                                                ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
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0WO-US3499 1WO-US0655 1WO-US196 1WO-US196 1WO-US2177 1WO-US2177 1WO-US2177 7US-05926 7US-06328 7US-06318	705 - 06354 705 - 06354 705 - 06354 705 - 06318 705 - 06318 705 - 06410 705 - 06410	98US-082569P 98US-082569P 98US-082764P 98US-083704P 98US-083495P 98US-083499P 98US-083499P 98US-083499P 98US-084464P 98US-084640P 98US-084640P 98US-084640P 98US-08558P 98US-08558P 98US-08559P 98US-08558P 98US-08558P 98US-08558P 98US-08558P 98US-086023P 98US-086023P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P 98US-087208P
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PR 05-JUN-1998; 98US-088121P
PR 10-JUN-1998; 98US-088121P
PR 11-JUN-1998; 98US-088121P
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PR 17-JUN-1998; 98US-091632P
PR 17-JUN-1998; 98US-09163P
PR 18-JUN-1998; 98US-09163P
PR 26-JUN-1998; 98US-09163P
PR 26-JUN-199

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20000MO-US23328

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                                                                                                                                                22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                                                                              ATGRILIS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; transmembrane protein; cytostatic; gene Therapy; TNR-Agonist-Alpha; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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                                                               98.7%; Score 1101; DB 24; Length 382; 96.3%; Pred. No. 9.6e-104; ive 0; Mismatches 0; Indels 8.
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01-DEC-1998; 98WO-US21141.
01-DEC-1998; 98WO-US21141.
08-MAR-1999; 99WO-US052108.
14-MAY-1999; 99WO-US10733.
01-SEP-1999; 99WO-US10733.
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02-JAN-2000; 2000WO-US2851.
05-JAN-2000; 2000WO-US04414.
05-JAN-2000; 2000WO-US06414.
01-MAR-2000; 2000WO-US0661.
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   98US-099843P.
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98US-099741P.
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PR 10-JUN-1996 9805-08812P-
PR 11-JUN-1996 9805-08812P-
PR 12-JUN-1996 9805-0895-14P-
PR 12-JUN-1996 9805-0895-
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112 141 172 201 25 8 ESEDEÇKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISOFRNWYUD Gaps ., 8 Length 382; Indels Score 1101; DB 24; Pred. No. 9.6e-104;); Mismatches 0; 206 . . . 0 98US-098723P. 98US-098821P. 98US-098843P. 98US-09562P. 98US-099741P. 98US-099754P. Query Match 98.7%; Best Local Similarity 96.3%; Matches 206; Conservative (01-SEP-1998; 02-SEP-1998; 02-SEP-1998; 02-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998; ~ 22 53 82 113 142 173 202 8 6 8 S 8 g 8 6

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version 5.	sw model	2003, 16:05:39 ; S (wit 2214	5-09-887-855-2_COPY_22_227 115 ATGRLLSGQPVCRGGTQRPC	Gapext 0.5	258052604 residues	satisfying chosen parameters		0% 100% 45 summaries	PTREMBL_23:* Bp_archea:* Sp_abcteria:* Sp_tungi:* Sp_human:*	ate:*	<pre>pp_danelie: sp_bhage:* sp_lant:* sp_rodent:* sp_virus:*</pre>	<pre>sp_vertebrate:* sp_unclassified:* sp_vrivus:* sp_bacteriap:* sp_archeap:*</pre>	No. is the number of results predic greater than or equal to the score derived by analysis of the total s	SUMMARIES	ΩI	QBTAY8 Q96NF3 Q96NC5 Q9Z209	Q8C351 Q8BM17 Q8BVU2 Q9W6E1	Q61830 Q25199 Q9Y5P9 Q9UBG0 Q64449	8K4Q8

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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuut T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y.,
Kawai Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
Isogai T.;
"NEDO human cDNA sequencing project.";
EMBL, AROSS654; BAB70978.1; -.
InterPro; IPR001304; Lectin C.;
R InterPro; IPR001304; Lectin C.;
R RART; SM00034; CLECT; 1.
R SMART; SM00034; CLECT; 1.
R Pfam; PPF00559; Lactin C.;
R Pfam; PPF00559; Lactin C.;
R Pfam; PPF00559; Lactin C.;
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R Pfam; PPF00559; Nachalashi C.;
R RART; SM00034; CLECT; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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84.8%; Score 945.5; DB 11; Length 374;
Best Local Similarity 85.9%; Pred. No. 9.4e-83;
Matches 176; Conservative 9; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.6%; Score 1111; DB 4; Length 374; 99.5%; Pred. No. 1.1e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR01304; Lectin C.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS0041; C TYPE LECTIN 2; 1.
SEQUENCE 374 AA; 742435 MW; 298A8BA24FB04EIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LPEETQEEDTKKTFKESREAALNLAY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borowsky M.L., Hynes R.O.;
"Layilin, a novel talin-binding of c-type lectins, is localized in J. Cell Biol. 143:0-0(1998).
EMBL; AP093673; AAC68695.1; -. HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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Q9Z209
            a
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SEQUENCE FROM N.A.

Isbibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

Horida M., Fujimori K., Takiguchi S., Kusano J.,

Matanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H.,

Mamamoto J., Isono Y., Kawai-Hio Y., Saito H., Wakamatsu A., Ishii S.,

Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

Mimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakani B.,

Natuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKOSSS9; BAR70946.1; --

EMBL, ROSSS9; RAR70946.1; --

EMBL, AKOSS99; BAR70946.1; --

EMBL, AKOSS99; BAR70946.1; --

EMBL, AKOSS99; BAR70946.1; --

EMBL, AKOSS99; BAR70946.1; --

EMBL, AKOSS99; BAR70940.1; --

EMBL, AKOSS99; BAR70946.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ATGRILISGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
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OJUSC-2001 (TERMELE1. 19, Created)
01-DEC-2001 (TERMELE1. 19, Last sequence update)
01-MAR-2003 (TERMELE1. 23, Last annotation update)
Hypothetical protein FLJ31092.
Hypothetical protein FLJ31092.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteles; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Hypothetical protein.
SEQUENCE 374 AA; 42280 MW; BAE64E6BC9E56DCD CRC64;
                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ30977.
                                                                      181 LPEETQEEDAKKTFKESREAALNLAY 206
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Query Match

Best Loca Matches

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83

Gaps

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82

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64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFBEAKEACRRDGGOLVSIESEDEOKLIEK 63
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
Nature 420:563-573 (2002)
EMBL; AK031063; BAC27234.1;
SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 RVVSGQKVCFADVKHPCYKMAYFHBLSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                       Length 246;
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STRAIN=C57BL/6J; TISSUE-Head;
MPLINE=22354683; PubMed=12466851;
The FANT=22354683; PubMed=12466851;
The FANT=C2010 Consortium,
the RIKEN Genome Exploration Research Group Phase I & II 'Analysis of the mouse transcriptome based on functional of the mouse transcriptome based on functional harure 420:553-573 (2002).
Mature 420:553-573 (2002).
EMBL; AK076523; BAC36378-1; -.
SEQUENCE 292 AA; 32502 MW; 73E631C0714D54E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                       52.0%; Score 580; DB 11; 57.9%; Pred. No. 8.9e-48;
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57.9%; Pred. No. 1.1e-47;
tive 26; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                     26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seg
01-MAR-2003 (TrEMBLrel. 23, Last ann
                   STRAIN=C57BL/6J; TISSUE=Forelimb;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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Matches 110, Conservative
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                                                                                   143
                                                                                                                                                VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPA-VPSREAEGEETELTTPVL 181
                                                                                                                                                                             55 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPA-VPSREAEGEE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE=Lung;
MEDIAIN=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,70 full-length CDNAs.";
Nature 420:563-573(2002).
EMBL; AK086930; BAC39765.1; -.
                                                         3 GRLLS-----GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV
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QBEMIT
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1AYILIN homolog (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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Pred. No. 2.2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                           PEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
72.1%;
Best Local Similarity 79.8%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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204 TEPATPLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 TELTTPVL 181
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                                                                             84
                                                                                                                                                                                                                                                                    182
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                                                                                                                                             123
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81 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 MFQWNDDRCNMKNNFICK---YSDEKPAVPSREAEGEETELTTPVLPEETQE----- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TTPTTPGGCKEGWHLYKNK 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 YKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Gaps
                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Warayyota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 1456;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6;
MEDLINE=93043353; PubMed=1421407;
MEDLINE=93043353; PubMed=1421407;
Marris N., Rite M., Chang G., Ezekowitz R.B.;
"Characterization of the murine macrophage mannose receptor.";
Blood 80:2363-2373(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL 18 POTENTIAL.
CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
SEQUENCE 1456 AA; 165065 MM; 4EBD3F1B8619A594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z11974; CAA78028.1; -.
HSSP; P22897; 1EGG.
                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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25.9%; Pred. No. 3.4e-08;
tive 33; Mismatches 66
                                                                                                                                      PRT; 1456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---WNDINCGYPNNFICORHNSSINATAMP
                            1160 -IG-----KWNDVPCNYNLPYICK 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:97142; Mrc1.
InterPro; IPR000355; Antifreezell.
InterPro; IPR000562; FN Type II.
InterPro; IPR0001304; Lectin C.
InterPro; IPR000772; Ricin B lectin.
Pfam; PF00040; fn2; 1.
Pfam; PF00059; lectin c, 8.
Pfam; PF00559; Ricin B lectin; 2.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR00135; FNTYPEII.
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                                                                                                                                                                                                                                       Macrophage mannose receptor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0615; C_TYPE_LECTIN_1; 6. PROSITE; PSS0041; C_TYPE_LECTIN_2; 9. PROSITE; PSS00023; FIBRONECTIN_2; 1. PROSITE; PSS0231; RICIN_B_LECTIN, 1.
      133 GIGGPYMFQWNDDRCNMKNNPICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000995; FW Type II; 1.
SMART; SM00034; CLECT; 8.
SWART; SW00059; FW2; 1.
SWART; SW00458; RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.9%
Matches 53; Conservative
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                   Neurocan core protein.

Gallus gallus (Chicken).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=20309833; PubMed=10851024;
Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
"Coordinate Regulation of Cadherin and Integrin Function by the Chondroitin Sulfate Proteoglycan Neurocan.";
J. Cell Biol. 149:1275-1288(2000).
EMBL, AP116856, AAD24546.2;
HSSP; P08709; 1BF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 185; DB 13; Length 1; 34.7%; Pred. No. 7e-09; ive 18; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                  PRT; 1290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMO0445; LINK; 2.
PSO0010; ASX HYDROXYL; 1.
PSO0010; ASX HYDROXYL; 1.
PSO0041; C_TYPE_LECTIN_2; 1.
PSO0022; EGF_1; 2.
PSO1186; EGF_2; 1.
PSO1186; EGF_2; 1.
PSO1181; EGF_2; 1.
PSO1181; EGF_2; 1.
PSO1181; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P08709; 1BF9.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000152; BGF_2.
InterPro; IPR001438; BGF_1.
InterPro; IPR001438; BGF_11.
InterPro; IPR00509; BGF_11.
InterPro; IPR001599; IG-11ke.
InterPro; IPR00110; IG-11ke.
InterPro; IPR001306; IG_MIC.
InterPro; IPR001308; Link.
InterPro; IPR001308; Link.
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Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; X1ink; 2.
PKINTS; PR01010; EGFBLCOD.
PRINTS; PR010565; LINKMODULE.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom, PD000918; Link; 2. SMART; SM0032; CCP; 1. SMART; SM00034; CLECT; 1. SWART; SM0179; EGF CA; 1. SWART; SM0409; IG; 1. SWART; SM04495; LINK; 2.
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Best Local Similarity 34.7
Matches 50; Conservative
                                                                                                                  PRELIMINARY;
197 NQ--PEETHE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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09W6E1;
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67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISOFRNWYVDEPS---CGSEVCVV 123
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Sheikh H., Yarwood H., Adhwooth A., Isacke C.;

"Endol80, an endocytic recycling glycoprotein related to the
"Endol80, an endocytic recycling glycoprotein related to the
"Endol80, an endocytic recycling glycoprotein related to the
"Endol80, an endocytic recycling glycoprotein receptor.";

Li calls and macrophages and functions as a lectin receptor.";

J. Cell Sci. 113:1021-1012(2000).

REMBL, ART14838; AAD30280.1; -.

RICEPPO; IPR000156; FN Type II.

RICEPPO; IPR0001304; Lectin C.

RICEPPO; IRR00056; Lipocln C.R.

RICEPPO; IRR00056; Lipocln C. 8.

REMBL; PR00059; Lectin C. 8.

REMBL; RR000395; FN Type II; 1.

REMBLY RR000395; FN Type II; 1.

REMART; SR00034; CLECT; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dan "A urokinase receptor-associated protein with specific collagenbinding properties.",
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | | :: | | 484 IW----GPEG------RWNDSPCNQSLPSICKKAGQLSQGAAEEDHG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 176.5; DB 4; Length 30.4%; Pred. No. 5.4e-08; ive 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase receptor-associated protein UPARAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWART; SMO059; FN2; 1.
SWART; SM00458; RICIN; 1.
SWART; SM00458; RICIN; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 8.
PROSITE; PS00023; FTBRONECTIN_2; 1.
PROSITE; PS00213; LIPOCALIN; 1.
PROSITE; PS50231; RICIN_B_LECTIN; 1.
                                                                               MEDLINE=20148849; PubMed=10683150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LSGQPVC--RGGTQRPC----YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1504; PROCEATITSAP.
PRINTS; PRO1504; PROCEATITSAP.
Probom; PRO00019; PYCKE, I.
SWART; SM0019; PYKKE; I.
PROSITE; PS00119; PYKKE; I.
PROSITE; PS001017; PROTEIN 1; 2.
PROSITE; PS001017; PROTEIN KINASE ATP; I.
PROSITE; PS001019; PROTEIN KINASE TYR; I.
RROSITE; PS00109; PROTEIN KINASE TYR; I.
ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 1348 AA; 156916 MW; 77D2122093227FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                01-MAY-1999 (TTEMBLrel. 10, Last Sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
Tyrosine Kinase receptor.
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Last annotation update)
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                                                                                                                                                                                  PRT; 1348 AA
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955 CFKIFGFANEEKKSWQDARQACKGL 979
                                                                                                                                                                                                                                                  (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
InterPro; IPR001245; Pro kinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00059; lectin C; 4.
Pfam; PP00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y5P9;
01-NOV-1999 (TrEMBLrel. 12, C.
01-NOV-1999 (TrEMBLrel. 12, L.
01-MAR-2003 (TrEMBLrel. 23, L.
Endocytic receptor Endol80.
ENDO180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6087;
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                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                  RESULT 10
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384 SWQPF-----QGHCYRL-----QAEKRSWQESKRACLRGGGDLLSIHSMAELEFITKQIK 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 KQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAGIGGPYMFQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSWIGLNDRTV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 BRD-------FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHESG------R 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANTE-CSTBL/61; TISSUE-Cerebellum;
MEDLINE-22346631;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK082298; BAC38458.1; -.
NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCPI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 1479;
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                                  | Prodom; | Prodoms; | Pu Type | I; | 1. |
| SMART; | SM00034; | CLECT; | 8 |
| SMART; | SM00034; | FUZET; | 8 |
| SMART; | SM00059; | FN2 | I. |
| R SMART; | SM000456; | CTYPE | LECTIN | 1. |
| R PROSITE; | PS00006; | CTYPE | LECTIN | 1. |
| R PROSITE; | PS00003; | FIBRONECTIN | 2. |
| R PROSITE; | PS00023; | FIBRONECTIN | 2. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | PS00213; | LIPOCALIN; | I. |
| R PROSITE; | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.3%; Score 170.5; DB 11; Length Best Local Similarity 31.4%; Pred. No. 2.1e-07; Matches 48; Conservative 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 217 AA; 25949 MW; 5F1A6A57B05B76D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 15.2%; Score 169; DB 11;
Local Similarity 31.1%; Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 IW----GPEG------RWNDSPCNQSLPSICK 504
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             PRINTS; PRO0013; FNTYPEII
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MULINE-96355501; PubMed=8702911;
WU K., Yuan J., Lasky L.A.;
"Characterization of a novel member of the macrophage mannose receptor type C lectin family.";
Type C lectin family.";
Mulionally.";
EMBL: US6734; AAC57729.1;
EMBL: US6734; AAC57729.1;
HSSP; P02751; ZFN2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 15.8%; Score 176.5; DB 4; Length 1479; Local Similarity 30.4%; Pred. No. 5.4e-08; etc. 51; Conservative 25; Mismatches 57; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
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Last annotation update)
code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
EMBL; AR107292; AAF14192.1;
EMBL; AR014609; BAA31684.1; -.
HSSP; P02751; 2FN2.
INCEPPO: IPR001304; LeCitn_C.
INCEPPO: IPR001304; LeCitn_C.
INCEPPO: IPR001304; LeCitn_C.
INCEPPO: IPR000565; Lipocln_CytFABP.
INCEPPO: IPR0007072; Ricin_B_lectin.
Pfam; PF000609; Inctin_C; 8.
PRINTS; PR00013; FNTYPEII.
PRODOM; P0000995; FN Type_II; 1.
SWART; SW00034; CLECT; 8.
SWART; SW00034; CLECT; 8.
PROSITE; PS00015; CTYPE_LECTIN_1; 8.
PROSITE; PS00015; CTYPE_LECTIN_2; 8.
PROSITE; PS00013; FIBRONECTIN_2; 8.
PROSITE; PS00013; INPOCALIN; I.
PROSITE; PS0013; INPOCALIN; I.
PROSITE; PS0013; INPOCALIN; I.
PROSITE; PS00213; INFORMECTIN_2; 8.
PROSITE; PS00213; INFORMECTIN_1.
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InterPro; IPR00128; Cytochrome P450.
InterPro; IPR001128; Cytochrome P450.
InterPro; IPR0001304; Lectin C.
InterPro; IPR000566; Lipocln CytFABP.
InterPro; IPR000772; Ricin B_lectin.
Pfam; PF00040; fn2; ll.
Pfam; PF00040; fn2; ll.
Pfam; PR00059; lectin c; %
PRINTS; PR00356; ANTIFREEZEII.
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80 RRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP-SCGSEVCVVMYHQPSAPAGIGGPY 138
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OBK4Q8

1D Q8K4Q8

DG Q8K4Q8

DT 01-OCT-2002 (TERBLrel. 22, Created)

DT 01-OCT-2002 (TERBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TERBLrel. 23, Last sequence update)

DT 01-OCT-2002 (TERBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TERBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TERBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TERBLrel. 23, Last annotation update)

COLIECTION CL.PI.

GN COLECI2 OR CL.PI.

OCLECI2 OR CL.PI.

OCLECI2 OR CL.PI.

OCLECI2 OR CL.PI.

OCLECI2 OR CL.PI.

OCLECI3 (CAPACAGA CANTINGAE)

OCLECI3 (CAPACAGA CANTINGAE)

NOSI TAXID=10090;

RN SEQUENCE FROM N.A.

RA Obtani K., Suzuki Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y.,

RA Obtani K., Suzuki Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y.,

RA Obtani K., Suzuki Y., Eda S., Kawai T., Cagasawara M.,

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CDNA cloning of mouse CL-PI gene.";

RA Yoshida I., Wakamiya N.;

REMBL, ADA03434; BAC0523.1;

DR MGD; MGI:2152907; Coleci2.

DR MGD; MGI:2152907; Coleci2.

DR Ffam; PF00059; Loctin C.; I.

DR Ffam; PF00059; Loctin C.; I.

DR Ffam; PF00059; Loctin C.; I.

DR Ffam; PR00059; ANTIFREEZEII.

DR FFAM; FS00059; CIPPE LECTIN 1; I.

DR PROSITE; PS00041; C-TYPE LECTIN 1; I.

DR PROSITE; PS00041; C-TYPE LECTIN 1; I.

DR PROSITE; PS00041; C-TYPE LECTIN 2; I.

SQUENCE 742 AA; 91304 MW; I537C490E5911C45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.8%; Score 165.5; DB 11; Length 742;
Best Local Similarity 33.8%; Pred. No. 2.7e-07;
Matches 50; Conservative 17; Mismatches 54; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Obtani K., Suzuki Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y., Putani K., Suzuki Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y., Fukuoh A., Wakamiya N., Itabe H., Suzutani T., Ogasawara M., "CDNA cloning of mouse CL-P1 gene."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

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714 AGGWNDFQCDEINNFICE--KEREAVPS 739
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Tue Dec 23 09:37:15 2003

Q9xyx3 hydra magni Q8vif6 mus musculu Q8vif6 mus musculu Q8cj86 mus musculu Q8cj84 mus musculu Q91zx4 mus musculu Q91zx0 mus musculu Q91zx0 mus musculu Q9cy1 bungarus fa Q8cj91 mus musculu Q8cj94 mus musculu Q8cj94 mus musculu Q8cj94 mus musculu Q8cj94 mus musculu Q8cj93 mus musculu Q8cj92 mus musculu Q9cy13 odocoileus Q9cy16 bongarus mu Q9cy13 caenorhabdi Q9wi8 bungarus fa Q8cy1340 megabalanus

Q9XXX3 Q9XXX3 hydra Q8VIF6 Q8Vif6 mus O62623 O62623 bos to Q8CJ86 Q8CJ86 mus Q8BHK7 Q8DHK7 mus Q91ZW4 mus	158 14.3 311 11 Q9DBV4 Q9dBv4 158 14.3 325 11 Q9LZXO Q91ZXO 15.1 14.2 158 13 Q90M77 Q90w77 Q90w77 Q90w77 Q90w77 Q90w77 Q90w77 Q90w77	156 14.1 339 6 Q95244 Q95244 E Q95244 E Q95244 E Q95240 Q95240 E Q	155 14.0 323 11 QBCJ8B 155 14.0 1152 13 Q90WM2 154 13.9 322 11 QBCJ89	152 13.9 3.3 11 QBCU32 152.5 13.8 485 6 Q954G3 152 13.7 158 13 Q90WI6	151.5 13.7 652 4 QBIXKI 150.5 13.6 399 6 QBHY12 150 13.6 197 6 Q28008 149.5 13.5 158 11 QBUZK6	149.5 13.5 459 5 149 13.5 158 13 148.5 13.4 163 13 148.5 13.4 195 5	148.5 13.4 330 4 Q9NT67 ALIGNMENTS	SUL	Created) Last sequence update) Last annotation update) roduct.	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; RN [1]		InterPro, IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1. PROSITE; PS50041; C_TYPE LECTIN_2; 1.	SEQUENCE Query Match Best Local :	OY 1 GRLLSGOPVCRGGTQRPCYKVIYFHDTSRRLMFEEAKEACRRDGGQLVSIESEDEQKL.	OY 61 KEIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISOFRNWYVDEPSCGSEVC	OY 121 VMYHQPSAPAGIGGPYMPQWNDDRCNMKNNPICKXSDEKPAVPSREAEGEETELTTPVI
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model	Run on: December 22, 2003, 16:05:39; Search time 23.7687 Seconds (without alignments) 2214.797 Million cell updates/sec	Title: US-09-887-855-2_COPY_24_227 Perfect score: 1106 Sequence: 1 GRLLSGQPVCRGGTQRPCYKEEDAKKTFKESREAALNLAY 204	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 830525 segs, 258052604 residues	local number of fits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 100* Maximum Match 100* Listing first 45 summaries	S	4: sp human:* 5: sp_invertebrate:* 6: sp_mamal:* 7: sp_mhc:*	sp_phage: sp_phage: sp_phage: sp_plant: sp_rodent: sp_virus: sp_virus: sp_virus: sp_virus: sp_virus: sp_virus:	<pre>8p_rvirus:* 8p_bacteriap:* 8p_archeap:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID	Q8TAY8 Q8t Q96NF3 Q96 Q96NC5 Q96 Q92209 Q9 Q933509 Q9	580 52.4 246 11 QBBMI7 580 52.4 292 11 QBBVU2 185 16.7 1290 13 Q9WEE1 178.5 16.1 1456 11 O61830	177.5 16.0 1348 5 Q25199 176.5 16.0 1479 4 Q9YSP9 176.5 16.0 1479 4 Q9UBG0 170.5 15.4 1479 11 Q64449	169 15.3 217 11 Q8C4F8 Q8c4f8 mus 165.5 15.0 742 11 Q8C4Q8 Q8k4Q8 mus 165.5 15.0 742 11 Q8C979 Q8c979 mus

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61 KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV 120

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RESULT 3
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,

Otsuki T., Sato H., Wakamatsu A., 18hi S., Yamamoto J., 1sono Y.,

Rawai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamamita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waqatsuma M.,

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EMBL: AKO55654; BAB70978.1; -.

Shall: AKO55654; BAB70978.1; -.

Richeror, IPR001304; Lectin_C.

Rem: PP00059; lectin_C.

SARR: SM00034; CLECT; 1.

Rem: PP00150; CTYPE_LECTIN_Z; 1.

Rem: PP00150; CTYPE_LECTIN_Z; 1.

Rem: PP00150; CTYPE_LECTIN_Z; 1.

Rem: PP00150; CTYPE_LECTIN_Z; 1.

Red: PR05ITE; PS50041; CTYPE_LECTIN_Z; 1.

Red: PR05ITE; PS50041; CTYPE_LECTIN_Z; 1.
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"Layllin, a novel talin-binding transmembrane protein homologous with C-type lectins, is localized in membrane ruffles.";
J. Cell Biol. 143:0-0(1998).
EMBL, AF093673; AACG6695.1; -.
HSSP; P22897; 1EGG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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85.5%; Score 945.5; DB 11; Length 374;
Best Local Similarity 85.9%; Pred. No. 8.2e-83;
Matches 176; Conservative 9; Mismatches 19; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001304; Lectin C.
Pfam; PR00059; lectin c; 1.
PR08178; PS0014; CLECT; 1.
PR08178; PS0041; C TYPE LECTIN 2; 1.
SEQUENCE 374 AA; 42435 MW; Z98A8BA24FB04E1C CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 EETQEEDTKKFFKESREAALNLAY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EETQEEDAKKTFKESREAALNLAY 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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SEQUENCE FROM N.A.

In Fabibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

In Fabibashi T., Hizoka S., Murakawa K., Takiguchi S., Kusano.

Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

Watanabe M., Fujimori K., Tanai H., Ishida M., Ishii S.,

Wamanoto J., Isono Y., Kawai-Hio Y., Saito M., Wakamatsu A., Ishii S.,

Wamanoto J., Isono Y., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

Sulauki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Remil, ANGS5539; Bash70946.11; -.

Remil, PROS5539; Bash70946.11; -.

Remil, PROS5539; Bash70946.11; -.

Remil, PROS059; lectin_C; 1.

Remil PROS059; lectin_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ30977.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096NC5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypotherical protein FLJ31092.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 AA.
                                                                                                                                                                                                                           374 AA
                                      204
                                                                  PROSITE, PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                     PRT;
                                      EETQEEDAKKTFKESREAALNLAY
                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
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                                      181
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117 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVPSREAEGEETELT 175
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                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oŧ
                                                                                                                                                                                                                                                                                                                                         62 FIENLLP-----SDGDFWIGLERREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                                                                                               83 MLQNLTKPGTGISDGDFWIGLLRSGDGQT-SGACPDLYQWSDGSSSGFRNWYTDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                        23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573 (2002)
EMBL; AK076523; BAC36378.1;
SEQUENCE 292 AA; 32502 MW; 73E631C0714D54E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                Length 246;
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52.4%; Score 580; DB 11; Length cz.
c7 9%; Pred. No. 1e-47;
c7 9%; Pred. no. 1e-47;
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                                                                                                                                        EMBL; AK031063; BAC27234.1; -.
SEQUENCE 246 AA; 27394 MW; B972660C58267752 CRC64;
                                                                                                                                                                                                                                      40;
                                                                                                                                                                                              52.4%; Score 580; DB 11; 57.9%; Pred. No. 8.1e-48; iive 26; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUB=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
              STRAIN=C57BL/6J; TISSUE=Forelimb;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                         Query Match 52.4%
Best Local Similarity 57.9%
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 57.9
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 TPVLPEETQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 NQ--PEETHE 204
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                                                The FANTOM Consortium,
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                117
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Q8BVU2
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                             VMYHOPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPA-VPSREAEGEETELTTPVL 179
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           KFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=2234683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation (60,770 full-length CDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-type lectin protein MT75 homolog.

Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 AA; 23697 MW; AD9870B5957DD5AE CRC64;
                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
LAYILIN homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score by...,
Pred. No. 2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.6%; Score 803.5;
79.8%; Pred. No. 2e-
                                                                                                                                                                          204 PEETQKEDTKETFKESREAALNLAY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBBM17;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                  121
                                                                                                                                                     180
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             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                             Q8C351
Q8C351,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8BMI7
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RESULT 6

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79 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           866 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF---- 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 MFQWNDDRCNMKNNFICK---YSDEKPAVPSREAEGEETELTTPVLPEETQE----- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---WNDINCGYPNNFICORHNSINATAMP-----TTPTTPGGCKEGWHLYKNK 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 YKVIYFHDTSRRLNPEBAKEACRRDGGQLVSIESEDBQKLIEKFIENLLPSDGDFWIGLR
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 178.5; DB 11; Length 1456; 25.9%; Pred. No. 3.3e-08; tive 33; Mismatches 66; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6;
MEDILME=93043335; PubMed=1421407;
Harris N., Rits M., Chang G., Ezekowitz R.B.;
"Characterization of the murine macrophage mannose receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Super M.;

B. Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.

R. REMBL; Z11974; CAA78028.1; -.

R. RISP; P22887; IRGG.

R. RISP; P22887; IRGG.

R. InterPro; IPR002353; AntifreeZeII.

R. InterPro; IPR000352; FN TYPE II.

R. InterPro; IPR000362; FN TYPE II.

R. InterPro; IPR000772; Ricin_B_lectin.

R. Ffam; PR00040; fn2; 1.

R. Pfam; PR00059; Iectin C; 8.

PRINTS; PR00059; Ricin_B_lectin; 2.

R. PRINTS; PR00059; FN TYPE II; 1.

R. SWART; SM00059; FNZ; II.

R. PROSITE; PS00615; C TYPE_LECTIN 1; 6.

R. PROSITE; PS00623; FIBRONECTIN_2; 8.

R. PROSITE; PS00623; FIBRONECTIN_2; 8.

R. PROSITE; PS00623; FIBRONECTIN_2; 8.

R. PROSITE; PS00623; FIBRONECTIN_2; 1.

R. PROSITE; PS00623; FIBRONECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 18 POTENTIAL.
19 1456 MACROPHAGE MANNOSE RECEPTOR
1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;
                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                 PRT; 1456 AA
                                   1160 -1G-----KWNDVPCNYNLPYICK 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EDAKKTFKESREALNL 202
                                                                                                                                                                                                                                                                                                                                                Macrophage mannose receptor precursor.
131 GIGGPYMFQWNDDRCNMKNNFICK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 80:2363-2373(1992)
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es 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
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                                                                                                                                         RESULT 9

1061830

1061830

107 01-NM

101-NM

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                                                                                                                                                                                                                                                                                                             Neurocan core protein.
Gallus gallus (Chicken).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20309833; PubMed=10851024;
Li H., Leung T C., Hoffman S., Balsamo J., Lilien J.;
"Coordinate Regulation of Cadharin and Integrin Function by the Chondroitin Sulfate Protecglycan Neurocan.";
J. Cell Biol. 149:1275-1288(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.7%; Score 185; DB 13;
34.7%; Pred. No. 6.8e-09;
iive 18; Mismatches 42;
                                                                                                                                                                   1290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SW00032; CCF; 1.
SWART; SW00034; CLECT; 1.
SWART; SW00004; CLECT; 1.
SWART; SW000409; LGF CA; 1.
SWART; SW00409; LGF 1.
SWART; SW00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00011; C_TYPE_LECTIN_1; 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF 1; 2.
PROSITE; PS01187; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR00161; EGF_2.
InterPro; IPR00161; EGF_1.
InterPro; IPR001613; EGF_II.
InterPro; IPR00509; EGF_II.
InterPro; IPR00509; Ig-II.
InterPro; IPR003010; Ig-II.
InterPro; IPR003010; Ig-II.
                                                                                                                                                                                                                               Created)
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Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF116856; AAD24546.2; -. P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin c; 1.
Pfam; PF00084; usushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR00010; BGFBLOOD.
PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Conservative
                                                                                                                                                                      PRELIMINARY;
                       197 NQ--PEETHE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000538; L.
InterPro; IPR000436; Si
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like (SEQUENCE
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                                                                                                                 RESULT
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SO WHAT HE REAL HEAD OF A REAL HEAD

53; Gaps

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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NRFIENDLIKDNDKYWIGLNKIWNDYLKKNKR-----FEWSDNTYTÖFFNWI 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 QKLIEKFIENLLPSDGD-FWIGLRR-----REEKQSNSTACQDLYAWTDGSISQFRNWY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LSGQPVC--RGGTQRPC----YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NESE'S TAISE'S INCOM.

IN INCEPPO: IPR001309; Jectin C.

IN INCEPPO: IPR001309; PANCREATIS ac.

IN INCEPPO: IPR001345; Tyr_Dkinase.

IN INCEPPO: IPR001245; Tyr_Dkinase.

IN FAM: PF00059; PKINASE; 1.

IN PRINTS; PR01059; PKINASE; 1.

IN PRINTS; SM00134; CLECT; 4.

IN RART; SM00134; CLECT; 4.

IN SWART; SM00134; TyrKc, 1.

IN PROSITE; PS00015; TyrKc, 1.

IN PROSITE; PS00011; PROTEIN I; 2.

IN PROSITE; PS00107; PROTEIN KINASE ATP; 1.

IN PROSITE; PS00109; PROTEIN KINASE TYR; 1.

IN PROSITE; PS00109; PROTEIN KINASE TYR; 1.

IN PROSITE; PS00109; PROTEIN KINASE TYR; 1.

IN RPOSITE; PS00109; PROTEIN KINASE TYR; 1.

IN RPOSITE; PS00109; PROTEIN KINASE TYR; 1.

IN RP051TE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Reidling J.C., Miller M.A., Steele R.E.;
"Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type Lectin-like Extracellular Domains.";
J. Biol. Chem. 275:10323-10330(2000).
EMBL; L22612; AAA29218.2;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                 Tyrosine kinase receptor.
Tyrosine kinase receptor.
Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        519 TWQPDNNNGIESCVEMNYN------GWSDKECKVLNGFICK 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDEP--SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 154
                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%; Score 177.5; DB 5; 28.0%; Pred. No. 3.8e-08; tive 32; Mismatches 46;
                                                                                                                  PRT; 1348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1479 AA
  CFKIFGFANEEKKSWQDARQACKGL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20209407; PubMed=10744720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 101-MAR-2003 (TrEMBLrel. 23, 1Endocytic receptor Endol80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaric,
hes 47; Conservative
                                                                                                                  PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q9Y5P9;
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Q25199
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Matches
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                           A Sheikh H., Yarwood H., Ashworth A., Isaacke C.;

The control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H
Momura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dan M. urokinase receptor-associated protein with specific collagen-binding properties ";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 16.0%; Score 176.5; DB 4; Length 1 Similarity 30.4%; Pred. No. 5.3e-08; 51; Conservative 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Urokinase receptor-associated protein UPARAP.
MEDLINE=20148849; PubMed=10683150;
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384 SWQPF-----QGHCYRL-----QAEKRSWQESKRACLRGGGDLLSIHSMAELEFITKQIK 433
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                                                                                                                                                                                                                                                                                                                                                                             5 SGOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CSTBL/6J; TISSUB=Cerebellum;
MEDLINE-22184683; PubMed=12466851;
THE FANTOM Consortium,
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of Nature 420:633-8712002)
EMBL; AK082298; BAC38458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                         Query Match 15.4%; Score 170.5; DB 11; Length 1479; Best Local Similarity 31.4%; Pred. No. 2e-07; Matches 48; Conservative 22; Mismatches 48; Indels 35;
                R PRODOM; PRODOMOSS; FN TYPE_II; 1.

R SMART; SM00059; FN TYPE_II; 1.

R SMART; SM00059; FN TYPE_II; 1.

R SMART; SM00059; FN TYPE_III; 1.

R PROSITE; PS00086; CYTOCHROME P450; 1.

R PROSITE; PS00018; CTYPE_LECTIN_1; 3.

R PROSITE; PS00023; FIBRONECTIN_2; 8.

R PROSITE; PS00023; ILIDOALNIN_1.

R PROSITE; PS50021; ILIDOALNIN_1.

R PROSITE; PS50021; ILIDOALNIN, 1.

R PROSITE; PS60021; IRIN B LECTIN, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chondroitin sulfate proteoglycan 3 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 169; DB 11;
31.1%; Pred. No. 2.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 IW----GPEG------RWNDSPCNQSLPSICK 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 WNDVPCNYNLPYVCK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 WNDDRCNMKNNFICK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96355501; PubMed=8702911;
Wu K., Yuan J., Lasky L.A.;
"Characterization of a novel member of the macrophage mannose receptor type C lectin family.";
J. Biol. Chem. 271:21323-21330(1996).
ENBL; U56734; AACS2729-1; -.
HSSP; P02751; 2FN2.
HSSP; P02751; 2FN2.
HSSP; P02751; 2FN2.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 176.5; DB 4; Length 1479; 30.4%; Pred. No. 5.3e-08; Live 25; Mismatches 57; Indels 35;
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Last annotation update)
                                EMBL; AF107292; AAF141921; EMBL; AF107292; AAF141921; -
EMBL; AB014609; BAA11684.1; -
EMBL; AB014609; BAA11684.1; -
EMBL; AB014609; BAA11684.1; -
INCEPPO; IPR000566; Lipoclin cytFABP.
INCEPPO; IPR000566; Lipoclin cytFABP.
INCEPPO; IPR00072; Ricin B_lectin.
Pfam; PF00040; fn2; 1.
Pfam; PF00059; lectin c; 8.
PRNYTS; PR00039; FN TYPEII; 1.
PRODOM; P0000995; FN TYPEII; 1.
SWART; SW00059; FN TYPE LECTIN 1; SWART; SW00059; FN TYPE LECTIN 1; PROSITE; PS00041; C_TYPE LECTIN 1; PROSITE; PS00041; C_TYPE LECTIN 2; PROSITE; PS00043; FTBRONECTIN 2; 1.
PROSITE; PS00043; FTBRONECTIN 2; 1.
PROSITE; PS0013; LIPOCALIN; I.
PROSITE; PS0013; LIPOCALIN; I.
PROSITE; PS0013; LIPOCALIN; I.
FROSITE; PS0013; LIPOCALIN; I.
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InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001304; Lectin C
InterPro; IPR0007072; Ricin_B_lectin.
Pfam; PF00040; fn2; 1.
Pfam; PF00040; lectin_c; 8.
PRINTS; PR00356; ANTIFREEZELI.
code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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les 51; Conservative
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Matches
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78 RRREEKOSNSTACQDLYAWTDGSISQFRNWYVDEP-SCGSEVCVVMYHQPSAPAGIGGPY 136
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DOLLAIN K., SUZUKI Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y.,

DOLLAIN K., SUZUKI Y., Eda S., Kawai T., Kase T., Keshi H., Sakai Y.,

A PUKUON A., Sakamato T., Itabe H., Suzutani T., Ogasawara M.,

YOSHida I., Wakamiya N.;

T. "CDNA cloning of mouse CL-P1 gene.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RMD: MGD: MGI:2152907; Colec12.

RMD: MGI:2152907; Colec12.

RMD: MGI:2152907; Colec12.

RICE-PRO: IPR001383; AntifreezeII.

R InterPro: IPR001383; AntifreezeII.

PEAM; PR00155; ANTIFREEZEII.

DR PRINTS; PR00356; ANTIFREEZEII.

DR PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS00615; C TYPE LECTIN 2; 1.

DR RROSITE; PS00615; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%; Score 165.5; DB 11; Length 742; Best Local Similarity 33.8%; Pred. No. 2.6e-07; Matches 50; Conservative 17; Mismatches 54; Indels 27; Gaps
                                                                      PRT;
                                          PRELIMINARY;
Q8K4Q8
AC Q8K4Q8
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DT 01-OCT-2
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COLDECT:
COL
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Search completed: December 22, 2003, 16:13:30 Job time : 23.9687 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 22, 2003, 16:05:09; Search time 6.56161 Seconds

(without alignments)

1476.391 Million cell updates/sec
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1476.391 Million cell updates/
Title: US-09-887-855-5
Perfect score: 1115
Sequence: 1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O9cxm0 musculu	homod		m snm	hom	bos			_	homo sa		rattus	P13608 bos taurus		canis	mus mu	O89103 mus musculu	ratt	_			homod	mus m		gall			9		7	P20693 mus musculu	P98105 rattus norv	39
SOMERIES	ID	CHOD MOUSE	CHOD_HUMAN	MANR HUMAN	PGCN_MOUSE	PGCN_HUMAN	PGCV_BOVIN	PGCN_RAT	PGCV_RAT	PGCV_MOUSE	PGCV_HUMAN	PGCV_CHICK	CD93_RAT	PGCA_BOVIN	PGCA HUMAN	PGCA_CANFA	LEM2_MOUSE	CD93_MOUSE	PGCA_RAT	PGCB_BOVIN	CD93_HUMAN	CLF1_HUMAN	FCE2_HUMAN	PGCA_MOUSE	PGCB_MOUSE	PGCA_CHICK	LECG_TRIST	PGCB_RAT	LEC2_MEGRO	LEM1_RAT	LEM1_MOUSE	FCE2_MOUSE	LEM2_RAT	LEC3_MEGRO
	DB	; -	-	-	-	-	-	н	٦	-	Н	ч	н		-	٦	П					-											٦	-
	Length	273	273	1456	1268	1321	3381	1257	2738	3358	3396	3562	643	2364	2415	2333	612	644	2124	912	652	197	321	2132	883	2109	158	883	173	372	372	331	4	9
g p	Ouery Match	51.5		•	15.9	•		•			'n.	'n.	4.	•	4.	13.9	•		-				ص		'n			ų.	ë.	۳		12.7		
	Score	574	561.5	182	177	17	174.5	174	174	174	174	171	165	158.5	158.5	155.5	154.5	153.5	153.5	152	151.5	151	-	148.5	147	146	145	-	44	44	43	141.5	-	140.5
	Result No.	-	7	m	4.	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28			31		

P98131 bos taurus	P07714 homo sapien	P05047 sarcophaga	P23806 trimeresuru	P43025 mus musculu	Q95198 macaca mula	Q28768 papio hamad	P23132 bos taurus	P43137 mus musculu	P83300 anser anser	Q95235 pongo pygma	P98107 bos taurus
LEM1 BOVIN	PSPA_HUMAN	LECA_SARPE	IXA TRIFL	TETN MOUSE	LEM1 MACMU	LEM1_PAPHA	LITH BOVIN	LIT1 MOUSE	ACAL ANSAN	LEM1 PONPY	LEM2_BOVIN
н	,-4	-		-	٦	7	-	-	-	-	-
370	248	283	152	202	372	372	175	165	132	372	485
12.6	12.5	12.5	12.4	12.4	12.3	12.3	12.2	12.1	12.1	12.1	12.1
140	139	139	138.5	138.5	137.5	137.5	136	135	134.5	134.5	134.5

ALIGNMENTS

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EMBL; AF257472; AAL05981.1; -.
EMBL; AL163217; CAB90388.1; -.
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                                                                  Nature 405:311-319(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY.
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P22897;
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                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                          4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                    64 FIENLLP----SDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                        23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                 83 MLQNLTKPGTGISDGDFWIGLLRSGDGQT-SGACPDLYQWSDGSSSQFRNWYTDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20289799; PubMed=10830953; Matanabe H., Yada T., Pattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Groner Y., Soeda E., Ohki M., Takagi T., Sakki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=22074930; PubMed=12079284;
Weng L., Smits P., Wauters J., Merregaert J.;
Menlecular cloning and characterization of human chondrolectin, a novel type I transmembrane protein homologous to C-type lectins.";
Genomics 80:62-70(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                          . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09H9P2; 09HCV3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annoration update)
Chondrolectin precursor (Transmembrane protein MT75) (PRED12
                                                                                                                                                                                                                                / Match 51.5%; Score 574; DB 1; Length 273; Local Similarity 57.4%; Pred. No. 4.3e-44; les 109; Conservative 26; Mismatches 41; Indels 1
                                                                                                                 CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL).
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
N-LINKED (GLCNAC...) (POTE
                                                                                                                                                                                                     E052D933F244F4C7 CRC64;
EMBL; AK014255; BAB29226.1; -.
HSSP; P22897; 1EGG.
MGD; MGI:2179069; Chodl.
InterPro; 1PR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
RPROSITE; PS00615; CTYPE_LECTIN_Z; 1.
RPROSITE; PS50041; CTYPE_LECTIN_Z; 1.
Lectin; Transmembrane; GIycoprofein; Signal.
                                                                                                                                                                                     V -> W (IN REF. 2).
T -> K (IN REF. 2).
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                                                                                                                                                                                                            30303 MW;
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216
237
273
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238
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CHODL OR C21ORF68.
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                                                                                                                                           TRANSMEM
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Best Local (
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RAN Scharte W. Schon O. Desario A. Nieseschann L. Dagand E., AN Wehrmeyer S. Bock A., Niagee S., Hemis S. M. Sieseschann L. Dagand E., Mehrmeyer S., Borzym K. Gaddiner K., Nieseic D., Francis F., Herrisch W. S. Borzym K. Gaddiner K., Nieseic D., Francis F., Herrisch W. S. Borzym K. Gaddiner K., Nieseic D., Francis F., Herrisch W. S. Borzym K. Gaddiner K., Nieseic D., Francis F., Herrisch W. Garling C. B. Gaddiner K., Nieseic D., Francis F., R. M. Borzym K. Gaddiner K., Nieseic D., Francis F., Bar N. B. B. Borger G. C., Galine G. D., Shemmen C. M., Schlar G. D., R. Mauser R. D., Octoria I. S., Nager L. S., Sager C. M. S., Nieseic C. M., Schlar G. D., R. Malson R. S., Dodden I. W. Doorg T., Nak S. I., Mang J., Habir F., Dager G. M. C., Octoria I. S., Marra M. M., S. I., Mang J., Habir F., Dager G. M., Dager G. M., Dager G. M., Schlar G. S., Gader G. M., Doorg T., Nak S. I., Mang J., Habir F., Mang M. M., Mang M. M., Mang J., Habir F., Mang M. M., Mang M.
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64 FIENLLP----SDGDFWIGLRRREEKQSNSTACODLYAWTDGSISQFRNWYVDEPSCGS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
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MEDLINE=92112893; PubMed=1730714;

Taylor M.E., Bezouska K., Drickamer K.;

"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";

J. Biol. Chem. 267:1719-1726(1992).
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MEDLINE=20347275, PubMed=10779515,
Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=90124192; PubMed=2373685;
Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;
"Primary structure of the mannose receptor contains multiple motifs resembling carbohydrate-recognition domains.";
J. Biol. Chem. 265:12156-12162(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=93052405; PubMed=1294118;
Kim S.J., Ruiz N., Bazouska K., Drickamer K.;
"Organization of the gene encoding the human macrophage mannose receptor (MRC1).";
Genomics 14:721-727(1992).
                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
C-LINED (GLCNAC. ) (POTENTIAL)
F4890AAPB572A311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of a C-type carbohydrate recognition domain from the macrophage mannose receptor.";
                                                                                                                                                                                                                                                                                         50.4%; Score 561.5; DB 1; Length 273; 60.1%; Pred. No. 5.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 11, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen).
                                                                                                                                                                                                                                                                                                                               25; Mismatches 35; Indels
                                                                                                                       CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
Pfam; PF00059; lectin_c; 1.
SMART; SW00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Transmembrane; G_YCOproTein; Signal.
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                                                                                                                     22 273 CHG
22 216 EXT
217 237 POT
238 273 CYT
35 179 CYT
86 86 N-I
273 AA; 30431 MW; F
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                                                                                                                                                                                                                                                                                                            Similarity
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P22897;
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DOMAIN
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J. Biol. Chem. 275:21539-21548(2000).

-I-FUNCTION: MEDIATES THE ENDOCYTOSIS OF GLYCOPROTEINS BY MACROPHAGES. IN SEVERAL RECOGNITION AND UPTAKE PROCESSES.

-I-SUBCELLULAR LOCATION: Type I membrane protein.

-I-MISCELLANEOUS: CRDS 1-3 HAVE AT MOST VERY WEAK AFFINITY FOR CARBOHYDRATE. CRD 4 SHOWS THE HIGHEST AFFINITY BINDING AND HAS MULTISPECIFICITY FOR A VARIETY OF MONOSACCHARIDES. AT LEAST 3 CRDS (4, 5, AND 7) ARE REQUIRED FOR HIGH AFFINITY BINDING AND RNDOCYTOSIS OF MULTIVALENT GLYCOCONJUGATES.

-I-SIMILARITY: CONCAINS 8 C-type lectin family domains.

-I-SIMILARITY: Concains 1 ricin B-type lectin domain.

-I-DATABASE: NAME=PROW; NOTE=PROW 2:85-89(2001);

WWM="http://www.ncbi.nlm.nih.gov/prow/quide/1641341515_g.htm".
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InterPro; IPR00353; Antifreezell.

InterPro; IPR00354; LeCin G: InterPro; IPR00374; LeCin G: InterPro; IPR00374; LeCin G: InterPro; IPR00372; Ricin B:lectin.

Pfam; PF00059; lectin G: 8. Pfam; PF00059; Ricin B:lectin; 2. Pfam; PF00059; Ricin B:lectin; 2. PRINTS; PR003595; FN TYPE-II: PRODOM; PR00995; FN TYPE-II: PRODOM; PR000995; FN TYPE-II: D. PR00095; FN T
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AAA603
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M93220; AAA60389.1;
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PDB: 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
GENEW; HGNI: 7228; MRCI.
MIM; 153618; -.
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M93215;
M93216;
M93217;
M93218;
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M93203;
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M93205;
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139 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----- 187
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                          ---WNDINCGYPNAFICORHNSSINATTVMP
                                                              978
                                              ------EDAKKTFKESREAAL 202
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000518; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00009; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X84727, CAA59216.1; -. PIR; S52781; S52781. HSSP, P00740; 1EDM. MGD; MG1:10464; CSPG3. InterPro; IPR000152; Asx_hydroxyl. InterPro; IPR000152; Asx_hydroxyl. InterPro; IPR000152; Asx_hydroxyl. InterPro; IPR000161; EGF_C3. InterPro; IPR001610; EGF_C3. InterPro; IPR001610; IGF_Ike.
                                                        |: :|:|:| 955 KCFKIFGFMEEERKNWQEARKACI
                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR01265; LINKMODULE.
PR00356; ANTIFREEZEII.
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Pfam; PF00084; sush; 1.
Pfam; PF00193; Xlink; 2.
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PRINTS; PR00356; ANTIFREEZ
ProDom; PD000918; Link; 2.
                                                                                                        STANDARD;
                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                                                            SEQUENCE FROM N.A
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Faessler R.;
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P55066;
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SMART; SM00059; FN2; 1.

SMART; SM00468; RICLY:

PROSITE; PS00615; C_TYPE_LECTIN_2; 8.

PROSITE; PS50041; C_TYPE_LECTIN_2; 8.

PROSITE; PS50031; FIGNONECTIN 2; 1.

PROSITE; PS50231; RICIN B LECTIN, 1.

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

North Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

PROSITE; PROSITE; PROSITE RECEPTOR;

POTENTIAL.
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C-TYPE LECTIN 1 (LONG FC
C-TYPE LECTIN 3 (LONG FC
C-TYPE LECTIN 4 (LONG FC
C-TYPE LECTIN 5 (LONG FC
C-TYPE LECTIN 5 (LONG FC
C-TYPE LECTIN 7 (LONG FC
C-TYPE LECTIN 7 (LONG FC
C-TYPE LECTIN 8 (LONG FC
C-TYPE LECTIN 8 (LONG FC
                                                                                                             CYTOPLASMIC (POTENTIAL)
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(GLCNAC...)
                                                                                                                       RICIN B-TYPE LECTIN.
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25.5%; Pred. No. 3.4e-08;
iive 37; Mismatches 61;
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Best Local Similarity 25.5
Matches 52; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-----TMPSVPSGCKEGWNFYSN 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and chromosomal localization of the mouse neurocan gene."; Genomics 28:405-410(1995).
-!- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- TISSUE SPECIFICITY: BRAIN.
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 2 Ink domains.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Sushi (SCR) domain.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C; TISSUE=Brain;
MEDLINE=96039250; PubMed=7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
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NCBI_TaxID=9606;
      1097 IGLNDRTVERD------FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHESG--- 1145
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                R SMART; SM00034; CLET; 1.

R SMART; SM001034; CLECT; 1.

R SMART; SM00109; EGF_CA; 1.

SMART; SM00109; IG; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00012; EGF_L; 2.

R PROSITE; PS00022; EGF_L; 3.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01241; LINK; 2.

R PROSITE; PS01241; LINK; 2.

M GJycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; GGF_Like domain; Calcium; Repeat; Lectin; Sushi; Signal.

T SIGNAL
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1G-LIKE V-TYPE.
LINK 1.
LINK 2.
EGF-LIKE 1.
EGF-LIKE 2.
C-TYPE LECTIN.
SUSHI.
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014554; Q9UPK6;
28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
CSPG3 OR NGAN OR NEUR.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches 49; Indels
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BY SIM
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SMART; SM00032;
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OR NEW YORK 
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1145 IGLNDRIVERD-----FQWTDNTGLQFENWRENOPDNFFAGGEDCVVMVAHESG--- 1193
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                                                                                                                                                                                                         EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50813; IG_LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGCV_BOVIN STANDARD, PRT; 3381 AA.
PB1262; 077609; 077610; 077611; 077612;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Chondroitin sulfate proteroglycan core protein groteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
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                                                                                   BGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal
SIGNAL 1 22 POTENTIAL.
                                                                                                                      NEUROCAN CORE PROTEIN.
IG-LIKE V-TYPE.
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BY LINKED (GLCNAC...
N-LINKED (GLCNAC...
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MEDLINE=98288320; PubMed=9624174;
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                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1075:248-258(1991).
-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P81282-4; Sequence=VSP 003078, VSP 003081;
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; the major isoform v2 is restricted to the central nervous system.

DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                    AND 342-348.
TISSUE-Spinal cord;
MEDLINE-92062692; PubMed=1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic
                                                                                                                                                                              SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zimmermann D.R.;
"Versican V2 is a major extracellular matrix component of the mature
bovine brain.";
M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SÜBUNIT: Interacts with FBLN1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P81282-3; Sequence=VSP_003080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P81282-1; Sequence=Displayed;
                                                                                                                  Biol. Chem. 273:15758-15764(1998)
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InterPro; IPR001742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR005209; EGF_like.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF066456; AAC24358.1; --
EMBL; AF060457; AAC24359.1; --
EMBL; AF066458; AAC24360.1; --
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IPR003006; Ig MHC.
IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000538;
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PIR; T42389; T42389
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Pfam;
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Gaps

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3162 QGQCYK--YF---AHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRV-----GHDYQ 3209
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3260 -----QMNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 3310
                                                                                                                                                                                                                                                                                                                                                                                                                       76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=94230574; PubMed=7513709;
MEDLINE=94230574; PubMed=7513709;
Margolis R.U., Grumet W., Karthikeyan L., Margolis R.K.,
Margolis R.U., Grumet M.
Margolis R.U., Margolis to the mourte of the mount of
                                                                                                                                                                                                                                                                                                                                               17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSED IN KIDNEY, LUNG, LIVER AND MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroltin sulfate proteoglycan 3)
(245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult core glycoprotein]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=99406907; PubMed=1326557;
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3311 KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 3361
                                                                                                                                                                                                                                                                                                              75;
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                                                                                                                                                                                                                                                                          DB 1; Length 3381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 ----ETELTT-----PVL----PEETQEEDAKKTFKESREAALN
     /FTId=vSP 003078.
Missing (In isoform V1).
/FTId=vSP 003079.
Missing (In isoform V2).
/FTId=vSP 003080.
Missing (In isoform V3).
/FTId=vSP 003081.
MISSING (IN REF. 2).
MISSING (IN REF. 2).
N -> D (IN REF. 2).
O -> D (IN REF. 2).
C -> R (IN REF. 2).
C -> R (IN REF. 2).
                                                                                                                                                                                                                                                                     ; Score 174.5; DB 1; Length 3; Pred. No. 4.5e-07; 26; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                       15.7%;
25.5%;
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1 20 POTENTIAL.
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EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
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                                                  Prodom; P0000318; Link; 2.
SWART; SM00032; CCP; 1.
SWART; SM0013; CCP; 1.
SWART; SM00179; EGE CA; 1.
SWART; SM00409; IG; 1.
SWART; SM00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; CTYPE LECTIN 1; 1.
PROSITE; PS00012; EGF 2; 1.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
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Pfam; PF00193; Xlink; 2.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR00356; ANTIFREEZEII.
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1037 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLISVHSPEEHKFINSF-----GHENSW 1085
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                                                                                                                    (GLCNAC. ) (POTENTIAL).

(XYL. .) (CHONDROITIN SULFATE).

(GLCNAC. ) (POTENTIAL).

(GLCNAC. ) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar Kyoto;
MEDLINE=9930804; PubMed=9642104;
Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding
proteoglycans in developing brain: aggrecan, versican, neurocan, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0), SEQUENCE FROM N.A. (ISOFORM V3), AND SEQUENCE OF 2657-2738 FROM N.A. (ISOFORM VINT) STRAIN=Wigtar Kyoto;
                                                                                                                                                                                                                              49; Indels 32;
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99ERB4; 008592; 008564; 03R1K4;
16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (FG-M) (Glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98094159; PubMed=9434070;
Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
"Proteoglycan expression in the normal rat kidney.";
Nephron 77:461-470(1997).
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                                                                                                          (POTENTIAL)
                                                                                                                                                                                                    Score 174; DB 1; Length 1257; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wight T.N.;
"Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                          992B33DCFA19EE1B CRC64;
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30.8%;
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
 CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein, Hyaluronic acid, Proteoglycan, Immunoglobulin domain, EGF-like domain, Calcium, Repeat, Lectin, Sushi, Signal.
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150 KDa ADULT CORE GLYCOPROTEIN.
11G-LIKE V-TYPE.
LINK 1.
LINK 2.
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Pfam; PF00184; sushi; l.
Pfam; PF00184; sushi; l.
Pfam; PF00184; sushi; l.
Pfam; PF00185; xlink; l.
PRINTS; PR00186; ANTIFREEZEII.
PRODEN; MO000318; Link; 2.
SWART; SW00034; CLECT; l.
SWART; SW00049; IG; ll.
SWART; SW00409; IG; ll.
SWART; SW00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; l.
PROSITE; PS000415; C_TYPE_LECTIN_1; l.
PROSITE; PS000415; C_TYPE_LECTIN_2; l.
PROSITE; PS001186; EGF_2; l.
PROSITE; PS01186; EGF_2; l.
PROSITE; PS01186; EGF_CA; l.
PROSITE; PS01186; EGF_CA; l.
PROSITE; PS01186; EGF_CA; l.
PROSITE; PS01186; EGF_CA; l.
                                                                                                                                                                                                                                                                                                        InterPro; IPR000153; Antifreezell.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0001642; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001801; IRE.
InterPro; IPR001801; IG-like.
InterPro; IPR001599; IG-like.
InterPro; IPR0010006; IG-MHC.
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InterPro; IPR000436; Sushi_SCR_CCP.
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Lectin_C.
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Pfam; PF00047; ig; 1.
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                   SEQUENCE OF 2535-2738 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
"Molecular cloning and characterization of two developmentally regulated genes in rat lung.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-: SUBUNIT: Interacts with FBLNI (By similarity).
-: SUBCELLULAR LOCATION: Secreted; extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 Eirlik domains.

SIMILARITY: Contains 2 Egr-like domains.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Sushi (SCR) domain.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoid=09ERB4-1; Sequence=VSP 001092;
TISSUE SPECIFICITY: In kidney is expressed in the papillary area, but not in glomeruli.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9ERB4-2; Sequence=VSP_003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=V0;
IsoId=Q9ERB4-1; Sequence=Displayed;
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EMBL, AF00454; AAD94544 1;

EMBL, AF072892; AAC26116.1;

EMBL, AY007691; AAC36631.1;

HSSP; P01132; 1EPG.

InterPro; 1PR001042; EGF Z.

InterPro; 1PR001042; EGF Z.

InterPro; 1PR001042; EGF Z.

InterPro; 1PR001043; EGF Z.

InterPro; 1PR001039; IG-Iike.

InterPro; 1PR001039; IG-Iike.

InterPro; 1PR001399; IG-IIK.

InterPro; 1PR00139; IG-IIK.

InterPro; 1PR00139; IG-IIK.

InterPro; 1PR00139; IG-IIK.

INTERPRO; IG-IIK.

INTERPO; IG-IIK.

INTERPRO; ITE-IK.

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76 WIGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
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PSAYORTYSKKYLKNSSSVKDNSINTSKHEHRWSRRWOETR
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/FTId=VSP 003092.
                                                                                                                                 GAG-ALPHA
(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
Hyaluronic acid; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2652
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                                                                                                                                                                          EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
SUSHI.
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2738 AA; 300004 MW; 12CA626D58BD8C6A CRC64;
                                                             VERSICAN CORE PROTEIN
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Name=V1;

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REQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).

RECUENCE OF 1-1692 FROM N.A. (ISOFORM V1).

RECUENCE STRAIN=CS7BL/6J; TISSUB=Skin;

REDINE=21085660; PubMed=11217851;

RA Kawan J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Babdan T., Banon H., Kaukawa T., Saito R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furun M., Anno H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujia M., Lee N.H.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hasebizaki Y.;

RA Nate 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 274:20444-20449(1999).
-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95181355; PubMed=7876137; Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human tissues."; J. Biol. Chem. 270:3914-3918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.; "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                          PGCV_MOUSE STANDARD; PRT; 3358 AA.
062059; 062058; 09CUU0;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel et al. 42, Last annotation update)
(Creation core protein precursor (Large fibroblast proteoglycan)
(Chodroitin sulfate proteoglycan core protein 2) (PG-M).
CSPG2.
                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
MEDLINE=91122551; PubMed=7822336;
ILO K., Shinomura T., Zako M., Ujita M., Kimata K.;
"Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).

    -!- SÜBUNIT: Interacts with FBLN1.
    -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
    -!- ALTERNATIVE PRODUCTS;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=4,
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q62059-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH FBLN1.
                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10400671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=V0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          versican.";
RESULT 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The Through are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
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lsoId=Q62059-2; Sequence=VSP_003087, VSP_003088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSICAN CORE PROTEIN.
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LINK 1.
LINK 2.
                                                                    IsoId=062059-3; Sequence=VSP_003089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:10288; CSpg2.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001152; Asx hydroxyl.
InterPro; IPR001181; EGF_Ca.
InterPro; IPR001181; EGF_Ca.
InterPro; IPR001181; EGF_Ca.
InterPro; IPR001199; IG_II interPro; IPR001180; IG_II interPro; IPR001180; IG_II interPro; IPR001180; IG_II interPro; IPR001180; IG_II interPro; IPR000180; IG_II interPro; IPR000180; IGF; 2.
InterPro; IPR000180; IGF; 2.
InterPro; IPR000180; IGF; 2.
InterPro; IPR000180; IGF; 3.
InterPro; IPR000190; IGF; 3.
InterPro; INK00119; IGF; 3.
InterPro; INK00119; IGF; 3.
INTERPRO; INK01180; IGF; 3.
INTERPRO; INK01180; IGF; 3.
INTERPRO; INTERPRO; 3.
I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D16263; BAA03796.1; -.
EMBL; D28599; -; NOT ANNOTATED_CDS.
EMBL; D32040; BAA066802.1; -.
EMBL; AXO14525; BAB29411.1; -.
HSSP; P01132; 1EPG.
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167
265
348
                                                                                                           Name=V3;
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(PG-M) (Glial

the human

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TISSUE=Lung fibroblast,
MEDLINE=88007514; PubMed=2820964;
Krushus T., Gehlsen K.R., Ruoslahti E.;
"A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90059882; PubMed=2583089;
Zimmermann D.R., Ruoslahti E.;
"Multiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mapping of the versican proteoglycan gene (CSPG2) to the long arm human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=95181355; PubMed=7876137;
MEDLINE=95181355; PubMed=7876137;
MEDLINE=95181355; PubMed=7876137;
MEDLINE=95181355; PubMed=7876137;
MEXPLESSION OF PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Aortic smooth muscle;
MEDLINE=99327053; PubMed=10397680;
Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95105187; PubMed=7806529;
Dours-Zimmermann M.T., Zimmermann D.R.;
A novel glycosaminoglycan attachment domain identified in alternative splice variants of human versican.";
J. Biol. Chem. 269:32992-32998(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                   MEDLINE=95105188; PubMed=7528742;
Naso M.F., Zimmermann D.R., Iozzo R.V.;
"Characterization of the complete genomic structure of th
versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perides G., Lane W.S., Andrews D., Dahl D., Bignami A., "Isolation and partial characterization of a glial hyaluronate-binding protein."; J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 251-347 FROM N.A.
MEDLINE=91122792; PubMed=1478664;
IOZZO R.V., NASO M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
         (Chondroitin sulfate proteoglycan core protein 2) hyaluronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT)
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J. Biol. Chem. 270:3914-3918(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY OF ISOFORMS.
MEDLINE=96213482; Pubmed=8627343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM V3).
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                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Glial tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
                                                                                                                                    NCBI_TaxID=9606;
           76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
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P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 15, Expense update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%; Score 174; DB 1; Length 3358;
28.5%; Pred. No. 5e-07;
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TVWNSNS -> QFGIQTA (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform V3)
/FTId=VSP_003090.
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(GLCNAC...)
(GLCNAC...)
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BY SIMILARITY.
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MISSING (IN REF. 3
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                                                                                                                                                                                                                                        Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
"Differential expression of versican isoforms in brain tumors.";
J. Neuropathol. Exp. Neurol. 55:28-313(1996).
-!-FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-!- SUBUNIT: Interacts with FBLNI (By similarity).
-!- SUBUNIT: Interacts with FBLNI (By similarity).
-!- ALTERNATIVE ROCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
-!- Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 118661; -.

GO; GO:0005578; C:extracellular matrix; TAS.

GO; GO:0005204; F:chondroitin sulfate proteoglycan; TAS.

GO; GO:0005240; F:chondroitin sulfate proteoglycan; TAS.

GO; GO:00052540; F:hyaluronic acid binding activity; TAS.

GO; GO:0007275; P:edevelopment; TAS.

R GO; GO:0007275; P:development; TAS.

R InterPro; IPR000182; Asx_hydroxyl.

R InterPro; IPR001829; EGF_Ca.

R InterPro; IPR001801; IG-Tike.

R InterPro; IPR001304; IG-Tike.

R InterPro; IPR001304; Lectin_C.

R InterPro; IPR001304; Lectin_C.

R InterPro; IPR001304; Lectin_C.

R InterPro; IPR000136; Sushi_SCR_CCP.
                                                                                                                                                                                                                      IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
                                                                                                                                                                          IsoId=Pl3611-2; Sequence=VSP_003082, VSP_003083;
                                                                                                                                                                                             IsoId=P13611-3; Sequence=VSP_003084;
                                                                                                                                              IsoId=Pl3611-1; Sequence=Displayed;
Name=Vl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U16306; AAA65018.1; --
EMBL, X15998; CAA34128.1; --
EMBL, S52488; AAB24878.1; --
EMBL; U2655; AAA67565.1; --
EMBL; D32039; BAA06801.1; --
EMBL; AC0414; AAA36437.1; --
PIR, S06014; A609455; AAD48545.1; --
PIR, S06014; A60973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00008; EGF; 2.
PF00059; lectin c; 1.
PF00084; sushi; 1.
PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:2464; CSPG2.
MIM; 118661; -.
                                                                                                                                        Name=V0;
                                                                                                                                                                                    Name=V2
                                                                                                                                                                                                           Name=V3
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Pfam;
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76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
SUSHI.
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SiGNAL 21 3396 VERSICAN CORE PROTEIN.
DOMAIN 21 146 IG-LIKE V-TYPE.
DOMAIN 167 244 LINK 1.
DOMAIN 265 346 LINK 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 3310
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Last sequence update)
Last annotation update)
SMART; SM00012; CCP; 1.
SMART; SM00014; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00109; IG; 1.
SMART; SM00145; LINK; 2.
PROSITE; PS00110; C_TYPE_LECTIN_1; 1.
PROSITE; PS0012; EGF_1; 2.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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                                                                                                      SEQUENCE FROM N.A. (ISOFORMS VO AND V1).
STRAIN=White leghorn; TISSUE=Limb bud;
MFDLINE=93300646; PubMed=8314802;
MFDLINE=93300646; PubMed=8314802;
Shinomura T., Nishida Y., Ito K., Kimata K.;
"CDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative spliced multiforms of PG-M and their relationships to versican.";
J. Biol. Chem. 268:14461-14469(1993).
-: FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                           Isold=Q90953-2; Sequence=VSP 003093;
TISSUE SPECIFICITY: Prechondrogenic condensation area of developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
Versican core protein precursor (Large fibroblast proteoglycan) (Chondroltin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 link domains.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-Additional isoforms seem to exist;
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IsoId=Q90953-1; Sequence=Displayed;
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EMBL, D13542; BAA02742.1; --
PIR; A47171, A47171.
HSSP, P00740; 1EDM.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000742; BGF_G.
InterPro; IPR001981; BGF_G.
InterPro; IPR001981; BGF_G.
InterPro; IPR00110; IG-like.
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Sushi_SCR_CCP.
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InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi SCP
Pfam; PFN00004
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InterPro; IPR001881; EC
InterPro; IPR006209; EC
InterPro; IPR007110; IC
InterPro; IPR003599; IC
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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                       PS00615, C TYPE LECTIN 1; 1...
PS00041; C TYPE LECTIN 2; 1...
PS00022; EGF 1; 2...
PS01186; EGF 2; 1...
PS01187; EGF CA; 1...
PS080835; IG LIKE; 1...
PS01241; LINK; 2...
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MEDINE=200508833, PubMed=10934210;

AMDINE=2050508833, PubMed=10934210;

AMDINE=2050508833, PubMed=10934210;

T lectin-like receptor with Structural homology to thrombomodulin.";

T lectin-like receptor with Structural homology to thrombomodulin.";

L. Misol. Chem. 275:34382-34392 (2000).

-!- FUNCTION: Receptor (or element of a larger receptor complex) for Clq, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and marchages upon interaction with solubbe defense collagens. May play a role in interactilular adhesion.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and heart. Expressed at lower level in brain, thymus, liver, spleen, intestine, kidney, adrenal gland, muscle and testis. Expressed on endothelial cells, platelets, undifferentiated monocytes and circulating natural killer cells.

-!- FTIM. N - and O-glycosylated (By similarity).

-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
3390 WIGL------NDKMFERDFRWTDGSPLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=PVG; TISSUE=Natural killer cells;
MEDLINE=20545218; PubMed=11093152;
Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
"Characterization and molecular cloning of rat ClqRp, a receptor on NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus:
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                          CD93_RAT STANDARD; PRT; 643_AA.

OPET61; O9JIZ6;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement component Clq receptor precursor (Complement component Subcomponent, IClqRp) (ClqR(p)) (Clq/MBL/SPA receptor)
CLO93 antigen) (Cell surface antigen AA4).
                                                                                                                                                                       : | | : : | | : | | : | | : | | : | | : : | | : : | | : : | | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                   132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO: 001601, C:integral to membrane; ISS. GO; GO: 001601; C:integral to membrane; ISS. GO; GO: 0016137; F:receptor activity; ISS. GO; GO: 0016137; P:cell-cell adhesion; ISS. GO; GO: 0005909; P:phagocytosis; ISS. InterPro; IPR00152, Asx hydroxyl. InterPro; IPR00181; EGF Ca. InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Immunol. 30:3355-3362(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF136537; AAG01572.1; -. EMBL; AF160978; AAF80402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells.";
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57 EQKLIEKFIENLL----PSD---GDFWIGLRRREEKQSNSTACQDLYAWT-DGSISQFRN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 EARHVQEALAQLLKTKAPSETKIGKFWIGLQREKGKCTYHDLPMKGFSWVGGGEDTTYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KWHESPCGTPDAPGNSIEGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGCA_BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; 028159;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
EGF-LIKE 1.
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL BEF-LIKE 4, CALCIUM-BINDING (POTENTIAL BY SIMILARITY.
B
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT COMPONENT CLQ RECEPTOR. EXTRACELLULAR (POTENTIAL).
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Pfam; PF00008; EGF; S.
Pfam; PF00008; EGF; S.
Pfam; PF00059; lectin c; 1.
SMART; SM00149; EGF CA; 3.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00018; CTYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01186; EGF 2; 3.
Cell adhesion; Receptor; Repeat, Signal; Transmembrane; EGF-like domain; Lectin; Glycoprotein.
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25.2%; Pred. No. 4.2e-07;
tive 35; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 WYKASKSŚCIŚKRĊVSLILDLSLKPHPSHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ICKYSDEKPAVPSREAEGEETELTTP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : : | | : | 178 LCKFNFKGMCSPLALGGPGQLTYTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68781 MW;
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Best Local Similarity
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-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 4 link domains.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 X 6 AA APPROXIMATE TANDEM REPEATS OF E-[EK]-P-F-P-S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
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SUSHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM01034; CLECT; 1.
SMART; SM01045; LINE; 4.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS000410; ASY_HYDROXYL; 1.
PROSITE; PS00042; C_TYPE_LECTIN_1; 1.
PROSITE; PS01049; EGF 1; 1.
PROSITE; PS01187; EGF 1; 1.
PROSITE; PS01187; EGF 1; 1.
PROSITE; PS01290; IG MHC; FALSE_NEG.
PROSITE; PS01291; LINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO00142; EGF_2.
InterPro; IPRO01801; EGF_Ca.
InterPro; IPRO01801; EGF_Ca.
InterPro; IPRO01801; IGF_Like.
InterPro; IPRO01001; IG_Iike.
InterPro; IPRO01006; IG_MHC.
InterPro; IPRO01004; Lectin_C.
InterPro; IPRO01038; Link.
InterPro; IPRO01038; Link.
InterPro; IPRO01039; Link.
InterPro; IPRO01031; Subhi_SCR_CCP.
Pfam; PPO0004; IGF; I.
Pfam; PPO01309; IGCF; I.
Pfam; PPO01309; IGCF; I.
Pfam; PPO01309; Subhi; I.
Pfam; PPO01309; Xink; 4.
PRINTS; PRO1265; LINKMODULE.
PRINTS; PRO0199; Xink; 4.
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LINK 2.
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LINK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07053; -; NOT_ANNOTATED_CDS.
PIR; A34234; A39808.
PIR; T42630; T42630.
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InterPro, IPR002353, Antifreezell.
InterPro, IPR00152, Asx hydroxyl.
InterPro, IPR00042; EGF_2.
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BY
BY
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THE STATE THE STATE STAT
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DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO
THE PROTECCLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE C-TERMINUS. GI CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                     Antonsson P., Heinegaard D., Oldberg A.;
"The kexatan sulfate-enriched region of bovine cartilage proteoglycan
consists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED (ABOUT 40) OLIGOSACCHARIDES.
PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN ADULT AND FETAL BOVINE PROTEOGLYCANS.
                Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea,
Bovidae; Bovinee, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87270630, PubMed=3111460, Oldberg A., Antonsson P., Heinegaard D., The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences arranged in homologous repeats.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perin J.-P., Bonnet F., Jolles J., Jolles P., "Sequence data concerning the protein core of the cartilage proteoglycan monomers. Characterization of a sequence allowing the synthesis of an oligonocleotide probe."; FEBS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Carrilage;
MEDLINE=93352525; PubMed=8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTI/L SEQUENCE.
MEDLINE=87005253; PubMed=3530809;
Perin J.P., Bonnet F., Jolles P.;
"Structural relationship between link proteins and proteoglycan
                                                                                                                                                                     SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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IsoId=P13608-1; Sequence=Displayed;
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MEDLINE=85027710; Pubmed=6489519;
                                                                                                                                                                                                                                                                                SEQUENCE OF 563-1056 FROM N.A.
MEDLINE=89380219; PubMed=2528543;
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ALTERNATIVE PRODUCTS:
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   2202 NN---NAQDYQWIGL-----NDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDC 2250
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                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2251 VVMIWHEKG-------EWNDVPCNYQLPFTCKKGTVACGEPPVVEHARIFGQKKD 2298
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01-APR-1990 (Rel. 14, Created)
01-AUG-1992 (Rel. 2) Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
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Baldwin C.T., Reginato A.M., Prockop D.J.;
"A new epidermal growth factor-like domain in the human core protein
for the large cartilage-specific proteoglycan. Evidence for
alternative splicing of the domain.";
J. Biol. Chem. 264:15747-15750(1989).
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MEDLINE=91093289; PubMed=1985970;
Doege K.J., Sasaki M., Kimura T., Yamada Y.;
"Complete coding sequence and deduced primary structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cartilage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms."; J. Biol. Chem. 266:894-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(POTENTIAL).
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TISSUBE-Chondrocytes;
Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                      (in isoform 2)
SP 003072.
                                                                                                                                                                                                                      (GLCNAC. . .)
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; Pred. No. 7.8e-06;
29; Mismatches 59;
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Best Local Similarity 26.8 Matches 48; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
-:- SIMILARITY: Contains 1 into domains.
-:- SIMILARITY: Contains 1 EGF-like domain.
-:- SIMILARITY: Contains 1 EGF-like domain.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
-:- SIMILARITY: Contains 1 Sushi (SCR) domain.
-:- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=P16112-3; Sequence=VSP 003074, VSP 003075; HODOMAIN: TWO GLOBULAR DOMAINS: G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROFEDCYAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSIGYS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, WOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFARE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                               MATRIX BIO. 14:323-328 (1994).

-!- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESISTS COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
-!- SUBUNIT: Interacts with FBLN1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                 Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005204; F:chondroitin sulfate proteoglycan; TAS.
InterPro; IPR002353; Antifreezell.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
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Comment=Additional isoforms seem to exist;
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                          TISSUE=Blood;
MEDLINE=95128522; PubMed=7827755;
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EMBL; J05062; AAA35726.1; -.
EMBL; X17406; CAA35463.1; -.
EMBL; S74659; AAC60643.2; -.
PIR; A39086; A39086.
HSSP; P98066; ITSG.
Genew; HGNC:319; AGC1.
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InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR003134; SGXXSG.
InterPro; IPR000436; Sushi_SCR.
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OF 764-864 FROM N.A.
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PF00059; lectin c; 1.
PF02339; SGXXSG; 71.
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ALTERNATIVE PRODUCTS:
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Matrix Biol. 14:323-328(1994).
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5 -> A (IN REF. 4).

5 -> A (IN REF. 2).

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P -> A (IN REF. 2).
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EGF-LIKE.
C-TYPE LECTIN.
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ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. BIOL. Chem. 268:17377-17383(1993).

-1- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGERNOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGIGLATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

-1- DOMAIN: TWO GLOBULAR DOWAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B, MOTIFE. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
                                                                                                                                                                                                                                                       9 QPVCRGG---TORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
PGCA_CANFA STANDARD; PRT; 2333 AA.

1D PGCA_CANFA STANDARD; PRT; 2333 AA.

C 028343; 028310;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-0CT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggrecan
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
VCBI_TaxID=9615,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 2082-2118 FROM N.A.
TISSUE=Cartilage;
MEDLINE=93352525; PubMed=8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel module."
                                                                                                       Match 14.2%; Score 158.5; DB 1; Length 2415; Local Similarity 29.1%; Pred. No. 8.1e-06; les 52; Conservative 22; Mismatches 62; Indels 43;
                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fueloep C.;
"Complete coding sequence and deduced amino acid sequence of
of canine cartilage.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cartilage;
MEDLINE=95128522; PubMed=7827755;
Barry F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the Keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
2391 2391 A -> P (IN REF. 2 AND 3).
2415 AA; 250191 MW; 1288937E1B98C6B6 CRC64;
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2003
          Copyright
```

protein search, using sw model OM protein - December 22, 2003, 16:06:34 ; Search time 10.0151 Seconds (without alignments) 1978.090 Million cell updates/sec Run on:

US-09-887-855-5 1115 1 ATGRLLSGQPVCRGGTQRPC.......BEDAKKTFKESREAALNLAY 206

Perfect score: Sequence:

BLOSUM62

Scoring table:

283308 segs, 96168682 residues Searched:

Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 76:*
1: pir1:*
3: pir2:*
: pir3:*

		df			SUMMAKIES	
Result	ć	Query		1	;	
	Score	Match	h Length	BB	QI	Description
	182	16.3	3 1456	Н	A36563	mannose receptor p
7	178.5		14	٦	A48925	
3	177		N	7	S52781	n - mouse
4	174.5		16	~	T14274	DZ
S	174.5	•	ന	7	T42389	
9	174		12	~	S28764	neurocan precursor
7	174	15.6	6 2397	-	A55535	
œ	174		24	Ч	A60979	versican precursor
6	171	15.3	35	~	A47171	
10	170.5	15.	14	~	T42710	mannose receptor.
11	158.5	14.	13	7	A39808	proteoglycan core
12	158.5	14.	23	7	T42630	addrecan - bovine
13	158.5	14.2	24	-4	A39086	aggrecan precursor
14	154.5	13.5		7	B42755	E-selectin precurs
15	153.5	13.8		7	A28452	proteoglycan core
16	152	13.6		7	A54423	brevican precursor
17	149.5	13.4		~	T24425	hypothetical prote
18	-4	13.4		Н	LNHUER	IdE Fc receptor II
19	148.5	13.3	3 330	7	T46256	brevican - human (
50	ന			-	A55182	aggrecan precursor
21	148		3 253	0	E89130	protein F52E1.2 (i
22			88	7	S57653	brevican precursor
23	146.5		16	Н	LNRC1	
24	-		210	Н	150421	addrecan precursor
25	145.5		7	7	JC7595	scavenger receptor
56	145		88	0	S49126	brevican precursor
27	4		17	7	S10548	
58	144.5	13.0		7	S23936	L-selectin precurs
59	144.5	13.0	404	7	A46274	inding

coagulation factor	L-selectin precurs	hypothetical prote	bitiscetin alpha c	phospholipase-A(2)	IGE Fc receptor,]	lectin BRA3-2 prec	L-selectin precurs	pulmonary surfacta	pulmonary surfacta	pulmonary surfacta	lectin precursor -	coagulation factor	tetranectin precur	hypothetical prote	igE Fc receptor II
JC4329	A32375	T26655	JC5058	S48719	LNMSER	LNRC3	S22124	LNHUPS	LNHUP6	LNHUP1	LNFHLS	JC4690	JC4031	T29200	S34198
ď	-	~	~	N	-	-	7		-	Н	٦	7	7	7	
129	372	463	131	1487	331	162	370	248	248	248	283	152	202	280	309
6	σ.	ο.	80.	۲.	۲.	9	9.	'n	'n	S	Ś	4.	4.	4	m.
12	12	12	12	12	12	12	12	12	12	12.5	12	12	12	12	12
143.5	143.5	143.5	142.5	142	141.5	140.5	140	139	139	139	139	138.5	138.5	138	137.5

ALIGNMENTS

```
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A36563; A60926; A44255; B44255; B44255; E44255; F44255; F44255; H4-SF, Conary, J.T.; Lennastc., M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A;Title: Primary structure of the mannose receptor contains multiple motifs resembling has the ference number: A36563; MUID:90324192; PMID:2373685
                                                                                                                                                                                                                                                                                                                                   A,Wolecule Lype: mRNA
A,Residues: 1-1456 <TAX>
A,Residues: 1-1456 <TAX>
A,Residues: 1-1456 <TAX
A,Residues: 1-1456 <TAX
A,Cross-references: GB:J05550; NID:g188675; PIDN:AAA59868.1; PID:g188676
A,Note: parts of this sequence, including the amino end of the mature protein, were con R. Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
A,Title: Molecular characterization of the human macrophage mannose receptor: demonstra A,Reference number: A60926; MUID:91079783; PMID:2258707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assetus: mucleic acid sequence not shown
Assetus: mucleic acid sequence not shown
Assetus: mucleic acid sequence not shown
Assetus: mucleic acid sequence is incomplete
Assetimes: GB:X55635
Associate in the authors translation additional residues Pro-Glu-Ile are shown after 497
Bs. Minote: muz. N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
Astitle: Organization of the gene encoding the human macrophage mannose receptor (MRCI)
Asteference number: A44255; MUID:93052405; PMID:1294118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary, nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: DNA
A;Residues: 155-233, 'KSAL', 238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865;
A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421
- human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:MRC1
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80 21 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR

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Query Match
16.3%; Score 182; DB 1; Length 1456;
Best Local Similarity 25.5%; Pred. No. 9.1e-08;
Matches 52; Conservative 37; Mismatches 61; Indels 5<

54;

Oy 188EDAKKTFKESREAALNL 204	Db 954 CFKIFGFANEEKKSWQDARQACKGL 978		SS2781 SS2781 Curcon - mouse	C.pdcute: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000 C.Accession: 552781	R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R. submitted to the EMBL Data Library, February 1995 A;Description: Amino acid sequence of mouse neurocan and brevican and their different A;Reference number. Se7281	A.Accession: S52781 A.Scriber S.	A;NOLGCULE CYPE: MKNA A;Residues: 1-1268 «RAU» A;Cross-references: EMBL:X84727; NID:q758629; PIDN:CAAS9216.1; PID:q758630	C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; F F;176-253/Domain: link protein repeat homology <lnk1> F;274-355/Domain: link protein repeat homology <lnk2> F;964-995/Domain: EGF homology <egf></egf></lnk2></lnk1>	F;1040-1160/Domain: C-type lectin homology <lch> F;1167-1223/Domain: complement factor H repeat homology <fhd></fhd></lch>	68;	Macches 45; Conservative 1/; Mismatches 49; Indels 32; Gaps 6; Qy 17 QRPCYKVIYFHDTSRRINFEEAKEACRROGGLVSIESEDEOKLIEKFIENLLPSDGDFW 76	on Db 1048 QGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSFGHENSW 1096	QY 77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAG 133	RCNMKNNFICK 156	ex Db 1146RWNDVPCNYNLPYVCK 1161	e RESULT 4	T14274 versionn precursor, splice form V2 - bovine C:Species: Bos priminanius raurus (rarria)	C;Date: 20.Sep-1999 #sequence_revision 20.Sep-1999 #text_change 05-May-2000 C;Accession: T14274	R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. J. Biol. Chem. 273, 15758-15764, 1998 A;Title: Versican V2 is a major extracellular matrix component of the mature bovine brackference number: Z17954; MUID:98288320; PMID:9624174 A;Accession: T14274	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1643 <sch></sch>	A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1 A;Experimental source: brain	Fireywords: giycoprotein Fil-16/JOpanis: signal sequence #status predicted <sig> Fi21-16/3/Proint: signal sequence #status predicted <mat> Fi21-16/3/Proint: versican, splice form V2 #status predicted <mat> Fi57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #s</mat></mat></sig>	. 11 ·	PCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 7
:: : : : : :	RREEKQSNSTA : :	866 ISLDKKFAWMDGSKVDYVSWATGEPNFANEDENCVTMYSNSGF 908	139 MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPEETQE 187	EDAKKTFKESREAAL 202	955 KCFKIFGFMEEERKUWQEARKACI 978	2 receptor precursor, macrophage - mouse	ss: Wus musculus (house mouse) 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	ion: AP925; S21320; PC245; N.; Super: M.; Rits, M.; Chang, G.; Ezekowitz, R.A.; 2363-2373; 1992 Characterization of the murine macrophage mannose receptor: demonstration that	since induper: A48925; MulD:93043353; PMID:1421407 18	le type: mRNA mes: 1-155 <abar mental source: peritoneal macronhage</abar 	sequence extracted from NCBI backbone (NCBIP:118733) , N.; Super, M.; Rites, M.; Chang, G.; Ezekowitz, R.B. ed to the EMBL Data Library. April 1992	ption: Characterization of the murine macrophage mannose receptor: Demonstration	nnce number: S21320 nion: S21320 : preliminary	.1e type: mkNA ces: 1-302, W',303-1117,'E',1119-1455 <haz> references: EMBL:Z11974: NID:GF2997. DIDN.CABARARA 1. DID.GE3000</haz>	, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Supe. Biophys. Res. Commun. 199, 682-692, 1994	The exon-intron structure and chromosomal localization of the mouse macrophage noce number: PC2245; MUID:94128116; PMID:8297379	Tou: FCLRYD: 1e type: mRNA es: 35-105 <ha3></ha3>	CS: MYC1 Airin A	A. Wady Dosition: Z. C. Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II is C. Keywords: membrane protein; receptor F.168-209/Domain: fibronectin type II repeat homology <2F9> F.368-268/Domain: C-type lectin homology <lch1> F.361-488/Domain: C-type lectin homology <lch1> F.341-488/Domain: C-type lectin homology <lch1></lch1></lch1></lch1>	Query Match 16.0%; Scott 18.5; DB 1; Length 1455;	Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;	21 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR 80 	81 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPY 138 	139 MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPEETQE 187

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C;Accession: A55535
R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
Biol. Chem. 270, 958-965, 1995
A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate A;Reference number: A55535; MUD:95122551; PMID:7822336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N'Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1257/Product: neurocan #status predicted <MAT>
F;23-1257/Product: neurocan #status predicted <MAT>
F;176-253/Domain: link protein repeat homology <LNK1>
F;176-253/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-G-D) motif
F;353-984/Domain: GF homology <B-D motif
F;1029-1149/Domain: C-type lectin homology <LCH>
F;1029-1149/Domain: C-mplement factor H repeat homology <FHD>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;1157-139,737,967,1164/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;344/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Contains: glial hyaluronate-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1037 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
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                                                                                                                                                                                                                                                                                                                                         Length 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----OWNDVPCNYHLTYTCKKGTVACGOPPVVENAKTFGK 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                      15.6%; Score 174; DB 2; 30.8%; Pred. No. 3.9e-07; iive 18; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.5%; Pred. No. 8.3e-
Matches 47; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RWNDVPCNYNLPYVCK 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 IGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       versican precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-2397 <RES>
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Versican precursor, splice form VO - bowine

NiAlternate names: chondroitin sulfate proteoglycan
C; Species: Bos primigenius taurus (cattle)
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C; Accession: T42389
R; Schmaffeldt, M; Dours zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A; Title: Versican V2 is a major extracellular matrix component of the mature bovine brain A; Reference number: Z17954; MUID: 98288320; PMID: 9624174
A; Reference number: Z17954; MUID: 98288320; PMID: 9624174
A; Residues: Dealiminary; translated from GB/EMBL/DDBJ
A; Residues: 1-3381 <SCH>
A; Residues: EMBL.AF060456; NID: 93253299; PID: 932533300; PIDN: AAC24358.1
C; Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin C; Reywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F; 1-20/Domain: signal sequence #status predicted <MAT>
F; 21-3381/Product: versican, splice form VO #status predicted <MAT>
F; 57,331,352,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2290,2356,26
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A;Ritle: Cloning and primary structure of neurocan, a developmentally regulated, aggreg A;Reference number: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
A;Accession: S28764
A;Accession: S28764
A;Accession: S28764
A;Accession: C-type lectin homology; Complement factor H repeat homology; C;Superfamily: aggrecan; C-type lectin homology; C;Reywords: chondroitin sulfate proteoglycan; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                            WIGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                            -----OWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                    1573 KDGFIORHLPTIRCLGNGRWAMPKITCLNPSAYORTYSKKYFKNSSSAKDN 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ** KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 3361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 3381;
                                                                                                                                                                                                                                                ---PVL----PEETQEEDAKKTFKESREAALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ETELTT------PVL----PEETQEEDAKKTFKESREAALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                      132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%; Score 174.5; DB 2;
llarity 25.5%; Pred. No. 1.1e-06;
Conservative 26; Mismatches 71;
                                                                                                                                                                                                                                                173 ----ETELTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                1472 WIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29,
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chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accssion: A47171
R;Shinomura, T; Nishida, Y; Ito, K; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBIP:134457)
core protein; C-type lecti
                                                                                                                                                                                                                                                                                                                                                                                      2238 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSAGEDCVVIIMHENG-- 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3390 WIGL------NDKMFERDFRWTDGSPLOYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
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N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                  17 ORPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 QRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:BAA02742.1; PID:g391644
                                predicted
                                                                                                                                                                                                                      Query Match 15.6%; Score 174; DB 1; Length 2409; Best Local Similarity 28.5%; Pred. No. 8.3e-07; Matches 47; Conservative 23; Mismatches 55; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.3%; Score 171; DB 2; Length 3562; 28.5%; Pred. No. 2.4e-06; ive 23; Mismatches 55; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2323
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A;Residues: 13562 c.SHI.
A;Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; EA;Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; EA;Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; EA;Cross-references: GB:D13542; NID:g391643; PiDS:Badence extracted from NCBI backbone (NCBIN:134456, NCS:Superfamily: chicken chondroitin sulfate proteoglycan PG-M:P:1664-345/Domain: link protein repeat homology cLNK2.
F:356-3327/Domain: EGF homology eGF1.
F:3358-33287/Domain: C-type lectin homology cLCH.
F:3461-3517/Domain: complement factor H repeat homology cFHD.
F;265-346/Domain: link protein repeat homology <LNK2>
F;539-1654/Domain: chondroitin sulfate attachment #status
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology <F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A47171; MUID: 93300846; PMID: 8314802
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A; Status: preliminary
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                                                                                           Western Petersor - Name and Condition sulfate proteoglycan 2 chondroitin sulfate proteoglycan 3 character dames appeared man appeared man ablema (man-lufflat) protein (1986-1986) and the condition of the condit
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aggrecan precursor, cartilage long splice form [validated] - human N'Allernate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; p N;Contains: aggrecan cartilage short splice form C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structural analy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1227 VVMIWHEKG------EWNDVPCNYQLPFTCKKGTVACGEPPVVEHARIFGOKKD 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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A;Cross-references: EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB38524.1
A;Experimental source: articular chondrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Bos primigenius taurus (cattle)
Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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            A; Reference number: A91327; MUID:85027710; PMID:6489519
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Best Local Similarity 26.8%
Matches 48; Conservative
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Best Local Similarity 26.8*
Matches 48; Conservative
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                                                      A; Accession: E29164
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C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage mannose receptor type C le
A;Tetle: Varacterization of A;Title: WID:9635501; PMID:8702911
A;Accession: T42710
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A;Molecule type: protein
A;Molecule type: protein
A;Recule 1,79: 74130;174-175,'A',177-204;208-225 <PER>
F;Pexin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protegolycan core protein, cartilage - bovine (fragments)
NyAlternate names: aggregating cartilage proteoglycan
NyAlternate names: aggregating cartilage proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C;Accession: A3434; A27752; A39808; A27751; E29164; B27751; C27751; D27751; F27
R;Antonsson, P.; Heinegard, D.; Oldberg, A.
A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of A;Reference number: A34234; MUID:89380219; PMID:2528543
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A;Residues: 128-621 <ANT>
A;Cross-references: GB:005028
R;Oldberg, A: Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from
A;Reference number: A27752; MUID:87270630; PMID:3111460
                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1479 <WUK>
A;Cross-references: EMBL:U56734; NID:g1336073; PID:g1336074; PIDN:AAC52729.1
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 SWOPF-----OGHCYRL-----QAEKRSWQESKRACLRGGGDLLSIHSMAELEFITKQIK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEVE---ELWIGL-----NDLKLÓMNFEWSDGSLVSFTHWHPFEPNNFRDSLEDCVT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE
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A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 622-1340 coLub>
R.Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
B. Biol. Chem. 266, 8198-8205, 1991
A.Title: Analysis of the catabolism of aggrecan in cartilage explants by A.Recession: A39808
A.Accession: A39808
A.Status: preliminary
A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 156
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A; Genes: GDB:AGC1; CSPGCP; MSK16
A; Cross-references: GDB:127479; OMIM:155760
A; Cross-references: GDB:127479; OMIM:155760
A; Cross-references: GDB:127479; OMIM:155760
A; Map position: 1526-15262
C; Map position: 1526-15262
C; Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracel F; 1-19/Domain: signal sequence #status predicted <SIG-F:1-19/Domain: signal sequence #status predicted <SIG-F:1-19/Domain: signal sequence #status predicted <SIG-F:1-150-2415/Product: aggrecan cartilage short splice form #status predicted <F:20-2162,2201-2319; A*. 2392-3415/Product: aggrecan short splice form #status predicted <F:21-2162,2201-2319; A*. 2392-3415/Product: aggrecan short splice form #status predicted <F:210-247/Domain: link protein repeat homology <LNK1>
F:268-349/Domain: link protein repeat homology <LNK2>
F:268-349/Domain: link protein repeat homology <LNK3>
F:593-673/Domain: link protein repeat homology <LNK3>
F:593-673/Domain: link protein repeat homology <LNK3>
F:677-861/Domain: link protein repeat homology <LNK4>
F:677-861/Domain: link protein repeat homology <LNK3>
F:671-861/Domain: chondroitin sulfate attachment #status predicted <CS1>
F:1511-2162/Domain: Edg Homology <LNK3>
F:1511-2162/Domain: Chondroitin sulfate attachment #status predicted <CS2>
F:1511-2162/Domain: Edg Homology <LNK3>
F:1516-2162/Domain: Edg Homology <LNK3>
F:1516-2162/Domain: Edg
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(Species: Mus musculus (house mouse)
(Space)
(Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;2332-2388/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #sta
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 OPVCRGG---TORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
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A;Residues: 1-612 <BEC>
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
R;Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992.
A;Title: Cloning of the mouse endothelial selectins. Expression of both E
A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%; Score 158.5; DB 1; Length 2415; 29.1%; Pred. No. 2e-05;
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A,Residues: 'MKATAGV',1-389,391-612 <WEL>
A,Cross-references: GB:M87862, NID:g193107
A,Experimental source: endothelial cells.
A;Note: sequence extracted from NCBI backbone (NCBIP:109470)
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Best Local Similarity 29.1%
Matches 52; Conservative
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               Concession, 20008; SDIOS, MANDS, SERVES, SERSES, SERVES, SERVE
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NyAlternate names: aggrecan
Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A23835; Ā28453; A28095; A28452
R;Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J:Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deductive conumber: A92623; MUID:88087070; PMID:3693370
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A;Residues: 1856-2124 <DO2>
A;Residues: 1856-2124 <DO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA1836.1; PID:g206105
R;Neame, J.; Christner, J.E.; Baker, J.R.
J. Blol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term
A;Reference number: A28453; MUID:88087071; PMID:3693371
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A;Residues: 20-37, W',39-60, E',62-64, X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A',
B;Residues: 20-37, W',39-60, E',62-64, X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A',
C;Superfamily: aggreean; C-type lectin homology; Excepted the factor H repeat homology; Excepted to a signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2124/Product: proteoglycan core protein #status predicted <WAT>
F;44-135/Domain: immunoglobulin homology <IMM>
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R;Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
A;Contents: annotation; revision to residue 698
A;Contents: annotation; revision to residue 698
R;Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial CDNA sequence encoding a globular domain at the C terminus of the rat A;Reference number: A23835; MUID:86250698; PMID:24248933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VNNVWIWVGTGKPLTEEAQNWAPGEPNNKQRNEDCVEIYIQRTKDSGM---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 YFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 YYNASSELMTYDEASAYCQRDYTHLVAIQNKEE---INYLNSNLKHSPSYYWIGIRK--- 76
F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: P-selectin #status predicted <MAT>
F;24-13-174/Domain: EGF homology <EGF>
F;143-174/Domain: Complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;243-300/Domain: complement factor H repeat homology <FH3>
F;363-426/Domain: complement factor H repeat homology <FH3>
F;368-426/Domain: complement factor H repeat homology <FH4>
F;314-489/Domain: complement factor H repeat homology <FH5>
F;349-548/Domain: complement factor H repeat homology <FH6>
F;35,391,528/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;266-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LK4>
F;2041-2034/Domain: Complement factor H repeat homology <FHD>
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Search completed: December 22, 2003, 16:14:42 Job time : 11.0151 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVWYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
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US-09-087-855-5
; Sequence 5. Application US/09807855
; Patent No. US20020058310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2803-US
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1115; DB 9;
Pred. No. 7.7e-105;
; Mismatches 0;
US-09-907-942-137
US-09-904-869-137
US-09-904-786-137
US-09-904-786-137
US-09-906-700-137
US-09-906-700-137
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US-09-907-925-137
US-09-905-081-137
US-09-902-634-137
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100.0%; Pr
tive 0;
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 ORGANISM: Homo sapiens
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 SEQ ID NO 5
LENGTH: 206
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 Query Match
Best Local S:
Matches 206
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                                                                                                                          ; Search time 19.6848 Seconds (without alignments)
1954.412 Million cell updates/sec
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1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-887-855-2
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                                                                                                                            December 22, 2003, 16:07:10
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                                                                                         OM protein - protein search, using sw model
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Maximum DB :
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61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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APPLICANT: TANG,
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LAL, Drug Aina M.
APPLICANT: LAL, Preeti
APPLICANT: AL-YOUNG, Janice
APPLICANT: AL-YOUNG, Janice
APPLICANT: AL-YOUNG, Janice
APPLICANT: No. 1
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: PP. 0760 PCT
CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2002-06-10
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 15
LENGTH: 374
                                                                                                                                                                                                                                                                                           22 ATGRILISGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEGKL
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US-10-149-819-15
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100.0%; Pred. No. 1.7e-104;
iive 0; Mismatches 0; ]
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Best Local Similarity 100.0%; Pred. No. 1.7e-104
Matches 206; Conservative 0; Mismatches 0;
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Publication No. US20030044913A1
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NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2090
LENGTH: 374
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                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-2090
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ORGANISM: Homo sapiens
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                                                                         Sequence 2, Application US/09887855
Patent No. US20020058310A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
FILE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MASCHAD, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
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Publication No. US20030219741A1
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Matches 206; Conservative
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OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-887-855-2
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121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                     61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGRLLSGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICANT: IRIE, RYOTARO
LICANT: TAMECHIKA, ICHIRO
LICANT: SEXI NAOHIKO
LICANT: YOSHIKAWA, TSUTOMU
LICANT: YOSHIKAWA, TSUTOMU
LICANT: YOSHIKAW, MOTOYUKI
LICANT: NAGAHARI, KENJI
LICANT: MASCHIO, YASUHIKO
LE OF INVENTION: NOVEL FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US,10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: 07 2001-0328381
PRIOR PELING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                        181 LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                            LPEETQEEDAKKTFKESREAALNLAY 206
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        OTSUKI, TETSULI
WAKAWATSU, AI
SATO, HIKOVUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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Matches 205; Conservative
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ORGANISM: Homo sapiens
US-10-094-749-2142
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; Sequence 137, Application US/09909320

RESULT 6 US-09-909-320-137

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IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/USO/04414
PRIOR APPLICATION NUMBER: PCT/USO/04414
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28664
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30999
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRI
ORGANISM: Homo sapiens
US-09-909-320-137
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CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                        Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
Ashkenazi, Avi
Botstein, David
                                                                                          Eaton, Dan L.
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EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 2000-01-05
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Matches 206; Conservative
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Eaton, Dan L.
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US-09-909-088B-137
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tudmas, Daniel
APPLICANT: Tudmas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,080B
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-09-18
PRIOR FILING DATE: 1999-09-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
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                                                                                                       1 ATGRLLS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                            Gaps
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          Length 382;
                                                       Indels
Query Match 98.7%; Score 1101; DB 10; Best Local Similarity 96.3%; Pred. No. 4.6e-103; Matches 206; Conservative 0; Mismatches 0;
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Patent No. US20020146709A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gaps

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,853

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/665,350

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03
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Grimaldi, Christopher J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
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Paoni, Nicholas F.
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                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                         Desnoyers, Luc
Eaton, Dan L.
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TYPE: PRT

CRGANISM: Homo Sapien

US-09-902-853-137
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR RILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-38

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07
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Matches 206; Conservative
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ORGANISM: Homo sapiens
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DB 10; Length 382; 98.7%; Score 1101; Query Match

US-09-902-853-137 ; Sequence 137, Application US/09902853 ; Publication No. US20020192659A1

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53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 382;
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Best Local Similarity 96.3%; Pred. No. 4.6e-103;
Matches 206; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLICATION NUMBER: PCT/US99/28564
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28665
PRIOR FILING DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 2000-01-05
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Roy, Margaret Ann
Stewart, Timothy A
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bustein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo Sapien US-09-907-824-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                              EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
                                                                                    1 ATGRLLS------GOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                                                                      22 ATGRILISASDLDIRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                       8; Gaps
                                    Indels
     96.3%; Pred. No. 4.6e-103; ative 0; Mismatches 0;
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PRIOR FLING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 90/665,350
PRIOR PLING DATE: 2000-02-18
PRIOR PLING DATE: 2000-02-22
PRIOR FILING DATE: 1099-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR FLING DATE: 1999-09-15
PRIOR FLING DATE: 1999-09-15
PRIOR FLING DATE: 1999-09-15
PRIOR FLING DATE: 1999-09-15
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5. US20020197671A1
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Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: Askbenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Earlon, Dan L.
APPLICANT: Ferrara, Napoleone
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Stewart, Timothy A.
Tumas, Daniel
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Kljavin, Ivar J.
Mather, Jennie P.
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Gerber, Hanspeter
Gerritsen, Mary E.
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     Best Local Similarity 96.3%
Matches 206; Conservative
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Publication No. US2(
GENERAL INFORMATION
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APPLICANT: TIMOLUY A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Woold, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: ACIG Encoding the Same
CURRENT PAPLICATION NUMBER: US/09/094,011
CURRENT PAPLICATION NUMBER: US/09/091414
PRIOR FILING DATE: 1090-00-18
PRIOR FILING DATE: 1090-00-22
PRIOR FILING DATE: 1090-00-22
PRIOR FILING DATE: 1090-00-22
PRIOR FILING DATE: 1090-00-22
PRIOR FILING DATE: 1090-00-30
PRIOR PAPLICATION NUMBER: PCT/US99/1240
PRIOR APPLICATION NUMBER: PCT/US99/1247
PRIOR APPLICATION NUMBER: PCT/US99/1240
PRIOR APPLICATION NUMBER: PCT/US99/1240
PRIOR APPLICATION NUMBER: PCT/US99/2001
PRIOR APPLICATION NUMBER: PCT/US99/2001
PRIOR PLING DATE: 1999-10-20
PRIOR PLING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: PCT/US99/2001
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-30
PRIOR PLING DATE: 1999-10
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                        Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart, Timothy A
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SEQ ID NO 137
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; ORGANISM: Homo Sapien
US-09-904-011-137
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PRIOR APPLICATION NUMBER: PCT/USO0/04414

PRIOR PELING DATE: 2000-02-25

PRIOR PELING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-05

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08-13

PRIOR FILING DATE: 1999-09-01-13

PRIOR FILING DATE: 1999-09-01-13

PRIOR FILING DATE: 1999-09-01-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-01-15

PRIOR PELING DATE: 1999-01-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-05

PRIOR PELING DATE: 1999-11-0
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
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22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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5. US20030003530A1
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US-09-904-011-137
Sequence 137, Applica.
Feducation No. US200300.
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
"PLICANT: Ashkenazi, Avi
"CANT: Botstein, David
"TANT: Desnoyers, Luc
"T. Eaton, Dan L.
"Tarara, Napole"
"Tarara, Napole
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Homo sapiens
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53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-11.

CURRENT APPLICATION NUMBER: US/09/906, 838

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18
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Pred. No. 4.6e-103;
0; Mismatches 0; Indels 8
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 137, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 96.3%;
Aatches 206; Conservative
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Gerber, Hanspeter
Gerritsen, Mary E
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: Williams, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT PELING DATE: 1000-00-18
RRIOR APPLICATION NUMBER: US/09/066,742
CURRENT FILING DATE: 2001-00-18
RRIOR APPLICATION NUMBER: US 60/143,048
RRIOR APPLICATION NUMBER: US 60/145,698
RRIOR APPLICATION NUMBER: US 60/146,222
RRIOR APPLICATION NUMBER: US 60/146,222
RRIOR APPLICATION NUMBER: US 60/146,222
RRIOR APPLICATION NUMBER: PCT/US99/20594
RRIOR APPLICATION NUMBER: PCT/US99/20309
RRIOR PILING DATE: 1995-09-15
PRIOR PLING DATE: 1995-09-15
PRIOR PLING DATE: 1995-10-05
RRIOR PLING DATE: 1999-10-05
RRIOR PLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
                          EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                  142 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNWRNNFICKYSDEKPAVPSREAEGE 201
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                           Sequence 137, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Geo, Wei-Olang
Gerber, Hanspeter
Gerittsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-02-22
RIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-06
PRIOR PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21089
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PLICATION NUMBER: PCT/US99/28113
PRIOR PLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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                                                                                                                                     Gerritsen, Mary E.
                                                                                                       Gerber, Hanspeter
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Mather, Jennie P.
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                                        Fong, Sherman
Sao, Wei-Qiang
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                                                                                                                                                                   Goddard, A.
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; ORGANISM: Homo sapiens
US-09-907-613-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                           PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-05
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PILICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PRILING DATE: 1999-09-01
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12
                       R FILING DATE: 2000-02-22

R APPLICATION NUMBER: US 60/143,048

R FILING DATE: 1999-07-07

R FILING DATE: 1999-07-26

R FILING DATE: 1999-07-28

R FILING DATE: 1999-07-28

R RELING DATE: 1999-07-28

R APPLICATION NUMBER: PCT/US99/20594
APPLICATION NUMBER: PCT/US00/04414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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Best Local Similarity 96.3
Matches 206; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-906-838-137
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US-09-907-613-137
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        53 ESEDEQKLIEKFIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYUD 112.

        Db
        82 ESEDEQKLIEKFIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYUD 141

        Oy
        113 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKUNFICKYSDEKPAVPSREAEGE 172

        Db
        142 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKUNFICKYSDEKPAVPSREAEGE 201

        Oy
        173 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206

        Db
        202 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 235

        Db
        202 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 235

        Job time: 20.6848 secs
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sarcophaga trimeresuru

macaca mula papio hamad musculu

POSO47 8 P23806 4 P43025 4 Q95198 4 P43132 4 P43132 4 P83300 6 Q95235 6 P98107 4

BOVIN MOUSE ANSAN PONPY

anser anser pongo pygma taurus

pog

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSTRAINCESTBL/GST. TISSUB=Embryonic head;

WEDLINE=2108560; PubMed=11217851;

REDLINE=2108560; PubMed S., Remanka I., Rondo S., Yamanaka I., Radica T., Saito R., Radica H.A., Ashburner M., Balarov S., Casavant T., Radica M., Matsud H.A., Radica B., Kochiwa H., Radica B., Kochiwa H., Radica T., Rashio T., Rashim M., Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G., Bakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G., Bakai K., Okido T., Pletcher C., Fullita M., Gariboldi M., Balake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ryons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Rymbhaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Rasahi Y., Rashi 
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEACURE CS7BL/6J;
STRAIN-CS7BL/6J;
Weng L., Smits P., Hubner R., Wouters J., Merregaert J.;
WH75, a low expressed c-type lectin gene involving in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chondrogenesis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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CHOD MOUSE STANDARD; PRT; 273 AA.
CHOCKMO; CHV131;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chondrolectin precursor (Transmembrane protein MT75)
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P16112 homo sapien
Q28343 canis famil
Q006590 mus musculu
089103 mus musculu
P07897 rattus norv
Q28062 bos taurus
Q9npy3 homo sapien
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1 RLLSGQPVCRGGTQRPCYKV......EEDAKKTFKESREAALNLAY 203
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        127863 seqs, 47026705 residues
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MANR HUMAN
PGCN MOUSE
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PGCV_RAT
PGCV_MOUSE
PGCV_HUMAN
PGCV_CHICK
CD93_RAT
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PGCA_HUMAN
PGCA_CANFA
LEM2_MOUSE
CD93_MOUSE
PGCA_RAT
PGCA_RAT
PGCB_BOVIN
CCD93_HUMAN
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PGCA MOUSE
PGCB MOUSE
PGCA CHICK
LECG TRIST
PGCB RAT
LECZ MEGRO
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LEMI_MOUSE
FCE2_MOUSE
LEM2_RAT
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Maximum Match 100%
Listing first 45 summaries
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LEC3_MEGRO
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
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MEDLINE-20289799; PubMed=10830953;

MEDLINE-20289799; PubMed=10830953;

Hartori M., Pujiyama A., Taylor T.D., Watanabe H., Yada T.,

Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Rosenchal A., Kudoh J., Shibuya K., Kawagaki K., Asakawa S.,

Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                        V -> W (IN REF. 2).
T -> K (IN REF. 2).
FRANCE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
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                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
EMBL, AK014255; BAB29226.1; -.
HSSP; P22897; LEGG.
MGD; MGI:2179069; Chodl
InterPro; 1PR001304; Lectin_C.
Ffam; PF00059; Lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Transmembrane; Glycoprofein; Signal.
SIGNAL
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                              TISSUB-EARAID;

WEDLINE=22388257; Pubbed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altauner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rodrish S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA, sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker H.,
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-1- PTM: N-glycosylated.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 27-273 FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.

Wagateuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.

Watanabe S., Kimura K., Murakami K., Ishili S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayamagi T.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blo
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dag,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                            1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                            23 RVVSGQKVCFADFKHPCYKMAYFHELSSRVSFQBARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                    61 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92112893; PubMed=1730714;
Taylor M.E., Bezouska K., Drickamer K.;
"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.
MEDLINE=20347275; PubMed=10779515;
Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MBDLINE=90324192; PubMed=2373685;
Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;
"Primary structure of the mannose receptor contains multiple motifs resembling carbohydrate-recognition domains.";
J. Biol. Chem. 265:12156-12162 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                7;
                                                                                                                                      CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-INKED (GLCNAC. . ) (POTENTIAL)
F4890AAPB572A311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93052405; PubMed=1294118;
Kim S.J., Ruiz N., Bezouska K., Drickamer K.;
"Organization of the gene encoding the human macrophage mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weis W.Ĭ.;
"Structure of a C-type carbohydrate recognition domain from the
macrophage mannose receptor.";
                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen).
                                                                                                                                                                                                                                              25; Mismatches 35; Indels
                                                                               POTENTIAL.
CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STUDIES ON THE BINDING OF INDIVIDUAL LECTIN DOMAINS
Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT.1.
PROSITE; PS000614; CTYPE_LECTIN_1; PALSE_NEG.
PROSITE; PS00415; CTYPE_LECTIN_2; 1.
Lectin; Transmembrane; Glycoprofein; Signal.
SIGNAL
CHAIN
22 273 CHONDROLECTIN.
DOMAIN 22 216 EXTRACELLULAR (POTE TRANSMEM 217 237 POTENTIAL.
DOMAIN 35 179 CTYPE LECTIN.
                                                                                                                                                                                                                  51.0%; Score 561.5; DB 1
60.1%; Pred. No. 5.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                    30431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor (MRC1).";
Genomics 14:721-727(1992).
                                                                                                                                                                                                                                                Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                  273 AA;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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ID MANR HUMAN
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                                                                                                                                                                                    SEQUENCE
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Genew, HGNC: 7228, MRC1.

R GATEW, HGNC: 7228, MRC1.

R GJ GO:0005887; C. integral to plasma membrane; TAS.
GO; GO:0005887; F:mannose binding activity; TAS.
R GO; GO:0006887; F:receptor activity; TAS.
R GJ; GO:0006889; P:receptor mediated endocytosis; TAS.
R RG; GO:0006899; P:receptor mediated endocytosis; TAS.
R InterPro; IPR000233; Antifreezell.
R InterPro; IPR00033; Antifreezell.
R InterPro; IPR00034; Lectin C.
R InterPro; IPR00077; Ricin B lectin.
R Ffam; PP00060; Ed2; Ricin B lectin.
R Ffam; PP00065; Ricin B lectin; 2.
R PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; RR00034; CLBCT; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | M93192; AAA60389.1; JOINED. |
| M93194; AAA60389.1; JOINED. |
| M93195; AAA60389.1; JOINED. |
| M93195; AAA60389.1; JOINED. |
| M93199; AAA60389.1; JOINED. |
| M93199; AAA60389.1; JOINED. |
| M93199; AAA60389.1; JOINED. |
| M93200; AAA60389.1; JOINED. |
| M93201; AAA60389.1; JOINED. |
| M93201; AAA60389.1; JOINED. |
| M93204; AAA60389.1; JOINED. |
| M93204; AAA60389.1; JOINED. |
| M93204; AAA60389.1; JOINED. |
| M93205; AAA60389.1; JOINED. |
| M93206; AAA60389.1; JOINED. 
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EMBL; M93221; AAA60389.1; -.
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AAA60389.1;
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PDB; 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
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M93219;
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EMBL;
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     136 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----- 184
                             909 ---WNDINCGYPNAFICQRHNSSINATTVMP-----TMPSVPSGCKEGWNFYSN 954
                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 28:405-410(1995).

-!- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and chromosomal localization of the mouse neurocan gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-i- SIMILARITY: Contains 2 EGF-like domains.
-i- SIMILARITY: Contains 2 link domains.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
-i- SIMILARITY: Contains 1 Sushi (SCR) domain.
-i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TISSUE=Brain;
MEDLINE=96039250; PubMed=7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
                                                                                                                                                          PRT; 1268 AA
                                                                          InterPro; IRRO01006; 19 MHC.
InterPro; IRR001004; Lectin_C.
InterPro; IRR001004; Link.
InterPro; IRR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
Pfam; PF00009; IQU.
Pfam; PF00009; Loctin_C; 1.
Pfam; PF00009; Loctin_C; 1.
Pfam; PF00109; Xink; 2.
PRINTS; PR01265; LINK40DULE.
PRINTS; PR00156; LINK4DULE.
PRINTS; PR00156; LINK4DULE.
PRINTS; PR00156; LINK4DULE.
PRODOm; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSR; S. PROTOTO; LEDM.
HSSEP, PROTOTO; LEDM.
MGD; MGI.104694; CBpg3.
InterPro; IPR001253; AntifreezeII.
InterPro; IPR001253; AntifreezeII.
InterPro; IPR001018; EGF 2.
InterPro; IPR001081; EGF 2.
R InterPro; IPR001801; EGF 1ike.
JR InterPro; IPR005299; EGF 1ike.
DR InterPro; IPR003599; Ig.
TherPro; IPR003599; Ig.
TherPro; IPR003006; Ig.MHC.
TherPro; IPR003006; Ig.MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - TISSUE SPECIFICITY: BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X84727; CAA59216.1; -. PIR; S52781; S52781.
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                      Rauch U., Gri
Faessler R.;
                                                                                                                                                        PGCN MOUSE
                                                          185
                                                                                                                                           MOUSE
                                                          δ
                                                                                  셤
                                                                                                                                                                       RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR 77
SMART; SM00059; FN2; 1.
SMART; SM00458; RICIN; 1.
PROSITE; PS000615; CTYPE LECTIN 1; 6.
PROSITE; PS00023; FÎBRONĒCTIN 2; 1.
PROSITE; PS50231; RICIN B LECTIN 2; 1.
PROSITE; PS50231; RICIN B LECTIN; 1.
POTENTIAL.
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16.5%; Score 182; DB 1; Length 1456;
Best Local Similarity 25.5%; Pred. No. 3.4e-08;
Matches 52; Conservative 37; Mismatches 61; Indels 5
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R SWART; SM00032; CCP; 1.

R SWART; SM00034; CLECT; 1.

R SWART; SM001034; CLECT; 1.

R SWART; SM001045; EGF CA; 1.

R SWART; SM001045; LINK; 2.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00011; C_TYPE_LECTIN_1; 1.

R PROSITE; PS001186; EGF 2; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS01187; EGF CA; 1.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19p12.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
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-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 2 Ink domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                         SEQUENCE OF 1-990 AND 1007-1321 FROM N.A.
Lamerdin J.B., McCready P.M., Skowronski E., Adamson A.W.,
Lamerdin J.B., McCready P.M., Skowronski E., Adamson A.W.,
Lamerdin J.B., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kryle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Langanan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attra C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.
Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of an -1 Mb region containing the MEF2B gene in
SEQUENCE FROM N.A.
MEDIJNE-99013874; PubWed-9795216;
MEDIJNE-99013874; PubWed-9795216;
MEDIJNE-99013874; Pennocchio L.A., Lieuallen K., Fan W., Lennon G.G.;
"Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
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SMART; SM00132; CCCP; 1.
SMART; SM00134; CLECT; 1.
SMART; SM00409; IG; 1.
SMART; SM00446; LINK; 2.
PROSITE; PS00010; ASX HVROXYL; 1.
PROSITE; PS00010; ASX HVROXYL; 1.
PROSITE; PS00012; C_TYPE LECTIN 1; 1.
PROSITE; PS00022; EGP 1; 3.
PROSITE; PS01186; EGF 2; 1.
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InterPro; IPR00188; BGF 2.
InterPro; IPR00188; BGF 1ike.
InterPro; IPR00110; IG-1ike.
InterPro; IPR003599; IG-
InterPro; IPR003599; IG-
InterPro; IPR001304; IG-
InterPro; IPR001304; IG-
InterPro; IPR000588; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00008; BGF; 2.
Pfam; PP00007; IG-1.
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EMBL; AC003110; AAB86655.1; -.
EMBL; AC00254; AAC2581.1; -.
HSSP; PO0740; IEDM.
Genew; HGNC:2465; CSPG3.
MIM; 600826; -.
InterPro; IPR000152; ABx_hydroxyl.
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ProDom; PD000918; Link; 2.
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Pfam; PF00059; lectin c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
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Pfam;
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS02141; LINK; 2.
PROSITE; PS02141; LINK; 2.
PROSITE; PS02141; LINK; 2.
EGP-coprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
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NEUROCAN CORE PROTEIN.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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P81282; 077609; 077610; 077612;
15-DEC-1998 (Rel. 37, Ceated)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-OCT-2011 (Rel. 42, Last annotation update)
16-OCT-2011 (Rel. 42, Last annotation update)
16-OCT-2012 (Rel. 42, Last annotation update)
16-OCT-2013 (Rel. 40, Last annotation update)
16-OCT-2013 (Rel. 4
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54 V -> A (IN REF. 2).
V -> A (IN REF. 2).
142972 MW; 2EF47F823DB980B8 CRC64;
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TISSUE=Forebrain;
MEDLINE=98288320; PubMed=9624174;
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31.5%; Pred. No. 1e-07
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                                         SOTITE STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=P81282-4; Sequence=VSP 003078, VSP 003081;
-:- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; he major isoform v2 is restricted to the central nervous system.
-:- DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                         SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
AND 342-348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: EDLONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                               TISSUE-Spinal cord;
MEDLINE-92062692; PubMed=1720020;
PELIGES G., Biviano F., Bignami A.;
PInteraction of a brain extracellular matrix protein with hyaluronic acid.";
                                                                  mature
                                                              "Versican V2 is a major extracellular matrix component of the
Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SÜBUNIT: Interacts with FBLNI (By similarity).
-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P81282-3; Sequence=VSP_003080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P81282-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1075:248-258(1991)
-!- FUNCTION: May play a role in intercel
                                                                                                                                    J. Biol. Chem. 273:15758-15764(1998)
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EMBL; AF060459; AAC24361.1; -.
PIR; T14274; T14474,
PIR; T42389; T42389.
HSSP; P01132; IEPG.
InterPro; IPR000152; A&x hydroxyl.
InterPro; IPR000152; EGF_2.
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EMBL; AF060458; AAC24360.1; --
EMBL; AF060459; AAC24361.1; --
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_11ke.
InterPro; IPR007110; Ig-Tike.
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PF00059; lectin c; 1.
PF00084; sushi; 1.
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                                  mmermann D.R.;
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3210 WIGL------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG-- 3259
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                                                                                                                                                                                                                                                                                                                                             14 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDBQKLIEKFIENLLPSDGDF- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=9420574; PubMed=7513709; Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K., Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K., Frumer M.; Friedlander M.; In the neuronal chondroitin W.; In the neuronal chondroitin wolfate proteoglycan neurocan binds to the neural cell adhesion molecules Ng-CAM/L1/NILB and N-CAM, and inhibits J. Cell Biol. 125:669 680 (1994).

J. Cell Biol. 125:669 680 (1994).

I. FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: BARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSED IN KIDNEY, LUNG, LIVER AND MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
(245 kDa early postnatal core glycoprotein) (Contains: 150 kDa adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=Spreague-Dawley, TISSUE=Brain,
MEDLINE=92406907; PubMed=1326557,
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroltin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19556-19547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-----
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                                                                                                                                                                                                                                                                  15.9%; Score 174.5; DB 1; Length 3381; 25.5%; Pred. No. 4.4e-07; ative 26; Mismatches 71; Indels 75;
                                        Missing (In isoform VI) /FIId=VSP 003079.
           FTId=VSP 003078
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                                                                                                                                                                                                                                                                                       Local Similarity 25.59
108 59; Conservative
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CSPG3 OR NCAN.
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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
GAG-BETA.
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and isoform V3)
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                                                                                                                                                                                                                                                                                                                Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.

1 POTENTIAL.

1 POTENTIAL.
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EGF-LIKE 2, CALCIUM-BINDING
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VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE.
LINK 1.
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SWART; SW00032; CCEC; 1.

SWART; SW00140; CLECT; 1.

SWART; SW00140; IGF CA; 1.

SWART; SW00140; IGF I.

SWART; SW00140; IGF I.

SWART; SW00140; IGF I.

SWART; SW00140; IGF I.

PROSITE; PS00110; CTYPE LECTIN I; 1.

PROSITE; PS0012; EGF I; 2.

PROSITE; PS01186; EGF Z; 1.

PROSITE; PS01186; EGF Z; 1.

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PRINTS; PR00356; ANTIFREEZEII.
ProDom; PD000918; Link; 2.
   PF00193; Xlink; 2
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).

PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL BRAIN, THE SNALL ISOFORM IS FOUND IN ADULT BRAIN.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 2 LGF-like domains.
SIMILARITY: Contains 1 L-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family similarity: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; BGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
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150 kDa ADULT CORE GLYCOPROTEIN.
IG-LIKE V-TYPE.
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SUSHI.
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PRINTS; PRO1365, ANTIFREEZEII.
PRODONO; PRO0366, ANTIFREEZEII.
SWART; SM00032; CCP; 1.
SWART; SM00034; CLECT; 1.
SWART; SM00199; EGF CA; 1.
SWART; SM00499; IG; 1.
SWART; SM00445; LINK; 2.
PROSITE; PS000445; LINK; 2.
PROSITE; PS00045; CTYPE LECTIN 1; 1.
PROSITE; PS00045; GTYPE LECTIN 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF 2; 1.
                                                                                                                                                                                                                                                                                  INCEPPO: IPRO02353; Antifreezell.
INCEPPO: IPRO0152; Asx hydroxyl.
INCEPPO: IPRO0162; BGF-Ca.
INCEPPO: IPRO01681; BGF-Ca.
INCEPPO: IPRO0209; BGF-Tike.
INCEPPO: IPRO0310; IG-Tike.
INCEPPO: IPRO03106; IG-Tike.
INCEPPO: IPRO0306; IG-Tike.
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Pfam; PP00004; ig; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 2.
Pfam; PF00193; Xlink; 2.
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HSSP; P00740; 1EDM.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%; Score 174; DB 1; Length 1257;
30.8%; Pred. No. 1.5e-07;
ive 18; Mismatches 49; Indels 32; Gaps
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MEDLINE=98308094; PubMed=9642104;
Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding
proteoglycans in developing brain: aggrecan, versican, neurocan, and
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G9ER84; 008592; 088564; QRRK4;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Chondroitin sulfate proteoglycan core protein proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
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Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
"Proteoglycan expression in the normal rat kidney.";
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                                                                                                                                                                                                                                                                                                                                                                                                                      135544 MW; 992B33DCFA19EE1B CRC64;
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                                       STRAIN-Sprague-Dawley; TISSUE-Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
regulated genes in rat lung.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May play a role in intercellular matrix. May take part in connecting caid.

-!- FUNCTION: May play a role in intercellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.

-!- SUBCELULAR LOCATION: Secreted; extracellular matrix.

-!- ALTERNATIVE PRODUCTS:

Comment-Additional isoforms seem to exist;

Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 link domains.

SIMILARITY: Contains 2 EGF-like domains.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Sushi (SCR) domain.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isold=09ERB4-3; Sequence=VSP 001092;
TISSUE SPECIFICITY: In kidney is expressed in the papillary area, but not in glomeruli.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9ERB4-2; Sequence=VSP_003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=09ERB4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF062402; AAC40166 1; --
EMBL, U75306; AAB51125.1; --
EMBL, AF084544; AAC46146.1; --
EMBL, AF084544; AAC4614.1; --
EMBL, AF087892; AAC4616.1; --
INTERPRO; IPR000142; EGF.2.
INTERPRO; IPR00189; EGF.2.
INTERPRO; IPR00189; EGF.1.
INTERPRO; IPR00189; IGF.1.
INTERPRO; IPR00189; IGF.1.
INTERPRO; IPR00189; IGF.1.
INTERPRO; IPR00189; IGF.1.
INTERPRO; IPR00189; IG.N.
INTERPRO; IPR00189; IG.N.
INTERPRO; IPR00189; IG.N.
SMART; SM00134; CCP; 1.
SWART; SM0019; EGF.CA; 1.
SWART; SM0019; EGF.CA; 1.
SWART; SM00149; IINK; 2.
PROSITE; PS0010; ASX HYDROXYL; 1.
PROSITE; PS001186; EGF.2; 1.
PROSITE; PS001186; EGF.2; 1.
PROSITE; PS01186; EGF.2; 1.
                     SEQUENCE OF 2535-2738 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Vint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=V3;
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2567 WIGL------NDKMFEHDFRWIDGSALQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSAYQRTYSKYLKNSSSVKDNSINTSKHEHRWSRRWQETR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Gaps
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                                                                                                                                                                                                                   GAG-ALPHA
(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
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BGF-like domain; Calcium; Immunoglobulin domain;
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; Pred. No. 3.8e-07;
23; Mismatches 55; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2652
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                                                                                                                                                                                                                                                                                           EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
SUSHI.
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2738 AA; 300004 MW; 12CA626D58BDBC6A CRC64;
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                                                                              VERSICAN CORE PROTEIN
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                                                                                                                                     IG-LIKE V-TYPE.
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N-LINKED
        Hyaluronic acid; Alternative splicing SIGNAL
                                                                                                                                                                                                                                                                          GAG-BETA
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Best Local Similarity 28.5%;
Matches 47; Conservative 2
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2486
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1660
11684
11738
11848
22004
22004
22711
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REALINE-C57BL/6J; TISSUE-Skin;

SEQUENCE OF 1-1692 FROM N.A. (ISOFORM VI).

STRAIN-C57BL/6J; TISSUE-Skin;

MEDLINE-21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., 'Okazaki Y., Gojobori T., Bono H., Kaukwa T., Satto R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.S., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,

K., Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki Y., Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
"Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
"Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
"Siol. Chem. 274:20444-20449(1999).
-!- FUNCTION: May play a role in intercellular signaling and in
connecting cells with the extracellular matrix. May take part in
the regulation of cell motility, growth and differentiation. Binds
hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95181355; PubMed=7876137; Zako M., Shinmata K.; Zako M., Shinomura T., Ujita M., Ito K.; Kimata K.; meression of PG-M (V.) an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                        PGCV_MOUSE STANDARD; PRT; 3358 AA.
062059; Q62058; O9CUU0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                     Ito K., Shinomura T., Zako M., Ujita M., Kimata K., multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.", J. Biol. Chem. 270:958-965(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÚBUNIT: Interacts with FBLN1.
SUBCELDULAR LOCATION: Secreted, extracellular matrix.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
MEDLINE=55122551; PubMed=7822336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=062059-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissues.";
J. Biol. Chem. 270:3914-3918(1995).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH FBLN1.
                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10400671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6;
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RESULT 9
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                                                                    ISOUG-062059-4; Sequence=VSP 003087, VSP 003090;
-1 TISSUB SPECIFICITY: V2 is found only in brain.
-1 DEVELOPMENTAL STAGE: Disappears after the cartilage development.
-1 SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1 SIMILARITY: Contains 2 EGF-like domains.
-1 SIMILARITY: Contains 1 Cetype lectin family domain.
-1 SIMILARITY: Contains 1 Cetype lectin family domain.
-1 SIMILARITY: Contains 1 Sushi (SCR) domain.
-1 SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein, Proteoglycan, Lectin, Extracellular matrix, Sushi, Signal, Repeat, EGF-like domain, Calcium, Immunoglobulin domain, Hyaluronic acid, Alternative splicing.
              Isold=062059-2; Sequence=VSP_003087, VSP_003088;
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IG-LIKE V-TYPE.
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                                           IsoId=Q62059-3; Sequence=VSP_003089;
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SWART; SMO0034; CLECT; 1.
SWART; SMO1034; CLECT; 1.
SWART; SMO1034; CLECT; 1.
SWART; SMO1040; IG; 1.
SWART; SMO0445; LINK; 2.
RROSITE; PSO0010; ASX HYDROXYL; 1.
RROSITE; PSO0041; C_TYPE_LECTIN_1; 1.
RROSITE; PSO1186; EGF_1; 2.
RROSITE; PSO1186; EGF_2; 1.
RROSITE; PSO1186; EGF_2; 1.
RROSITE; PSO1186; EGF_CA; 1.
RROSITE; PSO1186; EGF_CA; 1.
RROSITE; PSO1186; EGF_CA; 1.
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Sushi_SCR_CCP.
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LINK 2.
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EMBL; D28599; -; NOT ANNOTATED_CDS.
EMBL; D32040; BAA06802.1; -.
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InterPro; IPR000152; A8x hydroxyl.
InterPro; IPR00143; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR005209; EGF_like.
InterPro; IPR007110; IG-like.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_C
Pfam; PF00008; EGF; 2.
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Pfam; PF00084; sushi; l.
Pfam; PF00193; Xlink; 2.
PRINTS; PR01265; LINKMDULE.
ProDom; PD000918; Link; 2.
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Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung fibroblast;
MEDLINE=88007514; PubMed=2820964;
Krusius T., Gehlsen K.R., Ruoslahti E.;
A tibroblast chondroitin sulfate proteoglycan core protein contains lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                 TISSUB-placenta;
MEDLINE-90059882; PubMed=2583089;
Zimmermann D.R., Ruoslahti E.;
Multiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mapping of the versican proteoglycan gene (CSPG2) to the long arm human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                     the human
       (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP).
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MEDLINE=99327053; PubMed=10397680;
Lenire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Glial tumor;
MEDLINE=95105187; PubMed=7806529;
Bours=2simermann M.T., Zimmermann D.R.;
A novel glycosaminoglycan attachment domain identified in two alternative splice variants of human versican.";
J. Biol. Chem. 269:32998 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM V0).
MEDLINE=95.05188; PubMed=7528742;
MSDLINE=95.05188; PubMed=7528742;
MSDA M.F., Zimmermann D.R., Iozzo R.V.;
"Characterization of the complete genomic structure of th versican gene and functional analysis of its promoter.";
J. Blol. Chem. 269:32999-33008(1994).
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J. Biol. Chem. 264:5981-5987 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 251-347 FROM N.A.
MEDLINE=93122792; PubMed=1478664;
IOZZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
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MEDLINE=89174663; PubMed=2466833;
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MEDLINE=96213482; PubMed=8627343;
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                                                           Homo sapiens (Human)
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precursor (Large fibroblast proteoglycan)
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/FIId=VSP 003090.
A -> G (IN REF. 3).

MISSING (IN REF. 3).
I -> T (IN REF. 3).

TWWNSNS -> QFGIQTA (IN REF. 3).
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Pred. No. 4.9e-07;
23; Mismatches 55; Indels 4
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Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
"Differential expression of versican isoforms in brain tumors.";
J. Neuropathol. Exp. Neurol. 55:528-533 (1996).
-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=Pi3611-5; Sequence=VSP 003086;
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed in normal brain, gliomas, medulloblastomas, schwannomas, neurofibromas, and menningiomas; v2 is restricted to normal brain and gliomas; v3 is found in all these tissues except medulloblastomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
--- SIMILARITY: Contains 2 link domains.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Subh. (SCR) domain.
--- SIMILARITY: Contains 1 Subh. (SCR) domain.
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R EMBL; X15998; CAA34128.1; -.

R EMBL; S52488; AAB47851.1; -.

R EMBL; D32039; BAA67851.1; -.

R EMBL; D32039; BAA67851.1; -.

R EMBL; J02014; AAA36437.1; -.

R EMBL; AF00614; AAA36437.1; -.

R PIR; S06014; A6079.

R GGOW, GGOTC.2464; CSPG2.

R MIM; 118661; -.

R GO; GO:0005578; C:extracellular matrix; TAS.

R GO; GO:0005578; F:chondrotitin sulfate proteoglycan; TAS.

R GO; GO:000837; P:cell recognition; TAS.

R GO; GO:0008037; P:cell recognition; TAS.

R GO; GO:0008037; P:cell recognition; TAS.
                                                                                                                                                                     -!- SÜBUNIT: Interacts with FBLN1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                             IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P13611-3; Sequence=VSP_003084;
                                                                                                                                                                                                                                                                                                                    IsoId=P13611-1; Sequence=Displayed;
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InterPro; IPR001081; EGF 2.
InterPro; IPR001010; Ig-like.
InterPro; IPR003109; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR003106; Ig. MHC.
InterPro; IPR001306; Ig. MHC.
InterPro; IPR001304; Lectin.C.
IPEmn; PP00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Vint;
                                                                                                                                                                                                                                                                                              Name=V0;
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3225 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein, Proteoglycan, Lectin, Extracellular matrix, Sushi, Signal, Repeat, EGF-like domain, Calcium, Immunoglobulin domain, Hyaluronic acid, Alternative splicing.
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VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE.
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PGCV CHICK
ID PGCV CHICK STANDARD; PRT; 3562 AA.
10 PGCV CHICK (190945; 090945; 090945; 0100V-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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-ive 23; Mismatches
SMART; SM00022; CCP; 1.

SMART; SM00019; EGF_CA; 1.

SMART; SM01019; EGF_CA; 1.

SMART; SM00109; IG; 1.

SMART; SM00445; LINK; 2.

PROSITE; PS00610; ASX HYDROXYL; 1.

PROSITE; PS00610; C_TYPE_LECTIN_1; 1.

PROSITE; PS00022; EGF_1; 2.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.
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                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS VO AND V1).
STRAIN=White leghorn; TISSUE=Limb bud;
MFDLINE=93300846; PubMed=8314802;
Shinomura T., Nishida Y., Ito K., Kimata K.;
Shinomura T., Nishida Y., Ito K., Kimata K.;
"cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative spliced muliforms of PG-M and their relationships to versican.";
J. Biol. Chem. 268:14461-14469 (1993).
-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hypalizonic acid.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=Q90953-2; Sequence=VSP 003093;
TISSUE SPECIFICITY: Prechondrogenic condensation area of developing limb buds.

DEVELOPMENTAL STAGE: Disappears after the cartilage development
Versican core protein precursor (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).

EMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 link domains.

SIMILARITY: Contains 2 EGF-like domains.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                 SÜBCELLULAR LOCATION: Secreted; extracellular matrix ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing, Named isoforms=2, Comment=Additional isoforms seem to exist;
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InterPro; IPR00182; EGF_2.
InterPro; IPR001881; EGF_2.
InterPro; IPR001801; EGF_Tike.
InterPro; IPR005109; EGF_Tike.
InterPro; IPR005109; IG Tike.
InterPro; IPR003599; IG
InterPro; IPR003599; IG
InterPro; IPR003061; IG
InterPro; IPR001818; Sushi_SCR_CCP.
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Pfam; PF000194; sushi; 1.
Pfam; PF00193; Xilink; 2.
PRINTS; PR01265; LINKMODULE.
PRODOM; PD0000181; Link; 2.
SWART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
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                                                     Gallus gallus (Chicken).
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Pfam; PF00047; ig; 1
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NCBI_TaxID=9031;
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EGP-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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Matches 47; Conservative 23; Mismatches 55; Indels 40
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SEQUENTIAL SEQUENCE TISSUB-Lung;

MEDINE-20507883; PubMed-1034210;

Dean Y.D., McGreal E.P., Akatau H., Gasque P.;

Molecular and cellular properties of the rat AA4 antigen, a C-type of the recent of the rat AA4 antigen, a C-type of the recent of the rat AA4 antigen, a C-type of the recent of the rat AA4 antigen, a C-type of the recent of the rat AA4 antigen, a C-type of the rat AA4 antigen, a rate of the rat AA4 antigen, of the rat AA4 antigen, a rate of the rat AA4 antigen, of the rate of
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MEDLINE=20545218; PubMed=11093152;
Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
"Characterization and molecular cloning of rat CiqRp, a receptor on NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                   Q9ET61; Q9JIZ6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement component Clq receptor precursor (Complement component Clq receptor precursor (Complement Component Clq annotation (Complement Clq receptor ClqR(p)) (Clq/MBL/SPA receptor)
(CD93 annigen) (Cell surface antigen AA4).
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Eur. J. Immunol. 30:3355-3362(2000)
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InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF_like.
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                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACEMENT COMPONENT CLU RECEPTOR.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN.

EGF-LIKE 1.

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PSD---GDFWIGLRRREEKQSNSTACQDLYAWT-DGSISQFRNWY-VDEPSCGSEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VVMY-----HQPSAPAGIGGPYMFQWNDDRC-----NMKNNFICKYSDEKPAVPSR
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P13608; P79417; 028159;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
protein) (CSPCP).
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5e-07;
.hes 70; Indels 40; Gaps
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N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR
                                                                                                  SMART; SMO0034; CLECT; 1.

SMART; SMO0034; CLECT; 1.

SMART; SMO1179; BGF CA; 3.

PROSITE; PS00010: AŠX HYDROXVL; 3.

PROSITE; PS00101; C_TYPE_LECTIN_2; 1.

PROSITE; PS01186; BGF Z; 3.

PROSITE; PS01187; EGF CA; 3.

Cell adhealon; Receptor; Repeat; Signal; Transmembrane; BGF-like domain; Lectin; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENT COMPONENT C1Q
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InterPro; IPR001304; Lectin_C. Pfam; PP00008; EGP; 5. Pfam; PP000059; lectin_c; 1. SMART; SM00034; CLECT; 1. SMART; SM00179; EGP_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68781 MW;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
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DISULFID
DISULFID
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-1- SIMILARITY: Contains 1 immunoglobulin-like v-type domain.
-1- SIMILARITY: Contains 4 link domains.
-1- SIMILARITY: Contains 1 EGF-like domain.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 Sushi (SCR) domain.
-1- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROFECCIVCAN FAMILY.

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proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perin J.-P., Bonnet F., Jolles J., Jolles P.;
"Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligonucleotide probe.";
FEBS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                 proteoglycan,
                                                                                                                                                                                                                                                                                                                                                       TISSUB=Cartilage;
MEDLINE=93352525; PubMed=8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE.
MEDLINE=87005253; PubMed=3530809;
Perin J.P., Bonnet F., Jolles P.;
"Structural relationship between link proteins and proteoglycan
                                                                                                                                                                                                                                                 MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglyc
deduced from a cDNA clone, contains numerous Ser-Gly sequences
arranged in homologous repeats.";
                                                                                                                                                                       Antonsson P., Heinegaard D., Oldberg A.;
"The kexatan sulfate-enriched region of bovine cartilage r
"The kexatan sulfate-enriched region of bovine cartilage r
"The kexaten sulfate of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173 (1989).
                                                                                                       Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            dule.";
Biol. Chem. 268:17377-17383(1993).
                                                                                                                                              SEQUENCE OF 563-1056 FROM N.A.
MEDLINE-89380219; PubMed=2528543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=85027710; PubMed=6489519;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2114-2150 FROM N.A.
            Bos taurus (Bovine).
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
                                                                   NCBI_TaxID=9913;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein, Cartilage, Proteoglycan, Lectin, Signal,
EGF-like domain, Calcium, Alternative splicing, Repeat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
AGGRECAN CORE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINK 4.
23 X 6 AA APPROX
E-[EK]-P-F.
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Pfam; PF00049; 199; 1.

Pfam; PF00089; 190; 1.

Pfam; PF00089; 100; 1.

Pfam; PF00089; 100; 1.

Pfam; PF00089; 100; 1.

PRINTS; PR01265; LINKANDULE.

PRINTS; PR00036; ANTFREEZEII.

PROMODM; PD000318; Link; 4.

SMART; SM00032; CCP; 1.

SMART; SM00179; EGF CA; 1.

SMART; SM00179; EGF CA; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00012; EGF 1; 1.

PROSITE; PS000187; EGF CA; 1.

PROSITE; PS000187; EGF CA; 1.

PROSITE; PS00187; EGF CA; 1.

PROSITE; PS00187; EGF CA; 1.
                                                                                                                                                                                                                                     InterPro; IRR002353; Antifreezell.
InterPro; IRR000152; Asx_hydroxyl.
InterPro; IRR001042; EGF 2.
InterPro; IRR001881; EGF Ca.
InterPro; IRR00509; EGF like.
InterPro; IRR00110; Ig_like.
InterPro; IRR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                         Link. SGXXSG.
                                                                                                                                                                              EMBL; U76615; AAB38524.1; -.
EMBL; L07053; -; NOT_ANNOTATED_CDS.
PIR; A34234; A39808.
PIR; T42630; T42650.
HSSP; P08709; 1BF9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUSHI
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000538; Lin
InterPro; IPR003324; SGX
InterPro; IPR000436; Sus
Pfam; PF00008; EGF; 1.
Pfam; PF00047; ig; 1.
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2149
2344
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133
246
220
348
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504
602
774
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DOMAIN
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ISOId=P13608-2; Sequence=VSP 003072;
DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE C-TERMINUS. GI CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISGLETIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2

Event=Alternative splicing; Named isoforms=2;

Isold=P13608-1; Sequence=Displayed;

PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-

AND G3

+

LINKED (ABOUT 40) OLIGOSACCHARIDES.
PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
ADULT AND FETAL BOVINE PROTEOGLYCANS.

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| : |: |||| : |: ||2202 NN---NAQDYQWIGL------NDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDC 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGCA HUMAN STANDARD; PRT; 2415 AA.
P1612; Q13650;
01-APR-1990 (Rel. 14, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
AGCI OR CSPCI.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Chondrocytes;
MEDLINE-91093289; PubMed=1985970;
MEDLINE-91093289; PubMed=1985970;
Complete coding sequence and deduced primary structure of the human cartilage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms.";
J. Biol. Chem. 266:894-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).
MEDLINE=89380154; PubMed=2789216;
Baldwin C.T., Reginato A.M., Prockop D.J.;
"A new epidermal growth factor-like domain in the human core protein for the large cartilage-specific proteoglycan. Evidence for alternative splicing of the domain.";
J. Blol. Chem. 264:15747-15750(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.4%; Score 158.5; DB 1; Length 2364; Best Local Similarity 26.8%; Pred. No. 7.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6FF83763420C3D4C CRC64;
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Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.
CLINED (GLONAC...)
N-LINED (GLONAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform 2) /FTId=VSP_003072.
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2117
21182
22250
22281
2310
239
239
333
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 ISOId=P16112-3; Sequence=VSP 003074, VSP 003075; DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTROCINCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. GI CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULPIDE BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B, MOTIFS. GI IS SIMILAR TO G1. THE KERAPAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
 -I- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALIONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
-I- SUBUNIT: Interacts with FBLNI (By similarity).
-I- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
 CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
--- SIMILARITY: Contains 1 immunoglobuln-like V-type domain.
--- SIMILARITY: Contains 4 link domains.
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Sushi (SCR) domain.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
 TISSUB=Blood;
MEDLINE-9512852; PubMed=7827755;
BENTY F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
 MIM; 155760; -.

GO; GO:0005204; F:chondroitin sulfate proteoglycan; TAS.
InterPro; IPR00233; AntifreezeII.
InterPro; IPR005209; RGF like.
InterPro; IPR006210; IBGF.
 Event=Alternative splicing; Named isoforms=3; Comment=Additional isoforms seem to exist;
 IsoId=P16112-2; Sequence=VSP_003074;
 IsoId=P16112-1; Sequence=Displayed;
 Sushi_SCR_CCP.
 EMBL; M55172; AAA62824.1; -...
EMBL; J05062; AAA35726.1; -...
EMBL; X7406; CAA35463.1; -...
PIR, S74659; AAC60643.2; -...
PIR, A39086; A39086.
HSSP; P98066; ITSG.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
 aggrecan.";
Matrix Biol. 14:323-328(1994)
 SEQUENCE OF 764-864 FROM N.A.
 PF00059; lectin c; 1.
PF02339; SGXXSG; 71.
PF00084; sushi; 1.
PF00193; Xlink; 4.
 SGXXSG.
 Link.
 similarity).
 InterPro; IPR000538; Li
InterPro; IPR003324; SG
InterPro; IPR000436; Su
Pfam; PF00008; EGF; 1
 Name=3;
 Name=1
 AND G3
 Name=2
 Pfam;
 fam;
 Pfam;
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(POTENTIAL)
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 KS.
12 X APPROXIMATE TANDEM REPEATS.
CS-1.
29 X APPROXIMATE TANDEM REPEATS.
CS-2.
 and
 BY SIMILARITY.
BY SIMILARITY.
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CHOUNCE GLONAC...) (()
N-LINKED GLONAC...) (()
M-LINKED GLONAC.
 AND 3)
 AGGRECAN CORE PROTEIN
 -> A (IN REF. 4).
-> A (IN REF. 4).
-> A (IN REF. 2).
-> V (IN REF. 2 A.
 LINK 1.
LINK 2.
LINK 3.
LINK 3.
EGF-LIKE.
C-TYPE LECTIN.
 G-LIKE V-TYPE.
 G2-B.
G2-B'
 ဗ
 1497
2162
2162
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2198
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268
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772
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11;
 2253 NN---NAQDYQWIGL------NDRTIEGDFRWSDGHPWQFENWRPNQPDNFFAAGEDC 2301
 TISSUE-Cartilage;

MEDLINE-9332525; PubMed=8149621;

MATALINE-94 MATAL
 63 ENLLPSDGDF-WIGLRRREEKOSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 118
 2302 VVMIWHEKG------EWNDVPCNYHLPFTCKKGTVACGEPPVVEHARTFGQKKD 2349
 6 QPVCRGG----TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 62
 119 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 172
 PGCA_CANFA STANDARD; PRT; 2333 AA.

1D PGCA_CANFA STANDARD; PRT; 2333 AA.

C 28343; Q28310;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DF 15-SEP-2003 (Rel. 42, Last annotation update)

DB Aggrecan core protein precursor (Cartilage-specific proteoglycan core
 Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fueloep C.; "Complete coding sequence and deduced amino acid sequence of aggrecan of canine cartilage "; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 Gaps
 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
 43;
 14.4%; Score 158.5; DB 1; Length 2415; 29.1%; Pred. No. 7.9e-06; tive 22; Mismatches 62; Indels 43;
 TISSUE=Cartilage;
MEDINE=5912852; PubMed=7827755;
BBITY F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
 SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.,
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 2391 2391 A -> P (IN REF. 2 AND 3).
2415 AA; 250191 MW; 1288937E1B98C6B6 CRC64;
 aggrecan.";
Matrix Biol. 14:323-328(1994).
 SEQUENCE OF 774-833 FROM N.A.
 Best Local Similarity 29.1
Matches 52; Conservative
 SEQUENCE FROM N.A.
 NCBI_TaxID=9615;
CONFLICT
 Query Match
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us-09-887-855-2\_copy\_25\_227.rsp

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Search completed: December 22, 2003, 16:10:59
Job time : 7.46605 secs
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AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2 AND G3.

-!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
 AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
LINK 1.
LINK 2.
LINK 3.
LINK 4.
EGF-LIKE CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
G1-A.
G1-B.
G1-B.
G2-B.
KS.
 Glycoprotein, Cartilage, Proteoglycan; Lectin, Signal; Sushi;
EGF-like domain; Repeat; Immunoglobulin domain.
 SMART; SM00032; CCP; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00179; EGFCA; 1.

SMART; SM00179; EGFCA; 1.

SMART; SM00179; EGFCA; 1.

SMART; SM0010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00022; EGFL; 1.

PROSITE; PS01187; EGFCA; 1.

PROSITE; PS0187; EGFCA; 1.

PROSITE; PS00290; IG MHC; 1.

PROSITE; PS0187; EGFL; 1.
 EMBL; U65989; AAB66238.2; --
EMBL; S74662; AAC60527.1; --
InterPro; IPR001015; ABx hydroxyl.
InterPro; IPR001801; EGF 2.
InterPro; IPR001801; EGF 2.
InterPro; IPR001801; EGF 1.
InterPro; IPR001801; EGF 1.
InterPro; IPR001806; Ig_MHC.
InterPro; IPR000180; Ig_MT.
InterPro; IPR000180; IinterPro; IPR000180; Ilink; I.
Pfam; PF001809; EGF; I.
Pfam; PF001809; EGF; I.
Pfam; PF001809; EGF; I.
Pfam; PF001809; Idectin c; I.
Pfam; PF001809; Idectin c; I.
Pfam; PF001809; Interpro; IPR00180; IIINK; I.
PRINTS; PR001805; ANTIFREEEII.
PRODORS; PR00180; IINK; I.
 147
222247
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DOM: IN
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11;
 63 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 118
 62
 119 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 172
 6 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
 Query Match 14.1%; Score 155.5; DB 1; Length 2333; Best Local Similarity 28.5%; Pred. No. 1.4e-05; Matches 51; Conservative 24; Mismatches 61; Indels 43; Gaps
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 8B9ED78F3508B596 CRC64;
CS-1.

CS-2.

G3-2.

BY SIMILARITY.

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 N-LINKED (GLCNAC
N-LINKED (GLCNAC
 240573 MW;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein December 22, 2003, 16:06:34; Search time 9.86924 Seconds (without alignments) 1978.090 Million cell updates/sec Run on:

US-09-887-855-2 COPY 25 227

1100 - - -1 RLLSGQPVCRGGTQRPCYKV.....EEDAKKTFKESREAALNLAY 203 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | •                     |                    |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    |                   |
|-----------|-----------------------|--------------------|--------|---------|--------|--------|--------|--------|------|--------|------------------|-------------------|-------------------|--------|--------------------|-------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|-------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|
|           | Description           | mannose recentor n |        | - mouse | õ      |        |        |        |      |        | mannose recentor | proteoglycan core | addregan - howine | ċ      | E-selectin process | proteoglycan core | broadly can core | hymothetical prote | IGE En repentor II | brevican - himan ( | protein F52E1.2 (i | addregan precureor |         |       | addredan predireor | BCavender recentor | brevican predurent | Jectin - barnacle | L-selectin precure | HIV gp120-binding |
|           |                       | !                  |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    | •                 |
|           |                       | :                  |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    |                   |
|           |                       |                    |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    |                   |
| IES       |                       | :                  |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    |                   |
| SUMMARIES |                       |                    |        |         |        |        |        |        |      |        |                  |                   |                   |        |                    |                   |                  |                    |                    |                    |                    |                    |         |       |                    |                    |                    |                   |                    |                   |
| SUZ       |                       | A36563             | A48925 | \$52781 | T14274 | T42389 | S28764 | A55535 | 0979 | A47171 | T42710           | A39808            | T42630            | A39086 | B42755             | A28452            | A54423           | T24425             | LINHUER            | T46256             | E89130             | A55182             | \$57653 | LNRC1 | 150421             | JC7595             | 849126             | S10548            | \$23936            | 6274              |
|           | 8                     | A3                 | A4     | SS      | H      | T4     | S2     | A5     | A6   | A4     | T4               | A3                | T4                | A3     | B4                 | A2                | A5               | 12                 | 3                  | Ŧ.                 | E8                 | AS                 | SS      | Z     | 15                 | ÿ                  | SA                 | SI                | \$2                | A4(               |
|           | DB                    | -                  | -      | N       |        |        |        |        |      |        |                  |                   |                   |        |                    | ~                 | ~                | 7                  | Н                  | ~                  | ~                  | ٦                  | N       | ч     | Н                  | ~                  | ~                  | 7                 | 7                  | 7                 |
|           | Query<br>Match Length | 1456               | 1455   | 1268    | 1643   | 3381   | 1257   | 2397   | 2409 | 3562   | 1479             | 1340              | 2327              | 2415   | 612                | 2124              | 912              | 459                | 321                | 330                | 253                | 2132               | 883     | 162   | 2109               | 742                | 883                | 173               | 372                | 404               |
|           | ដូម                   | ľ.                 | ~!     |         |        | ٥.     | œ.     |        |      | ທຸ     | 'n               | 4.                | 4                 | 4      | ٥.                 | 0.                | 89.              |                    |                    | 'n                 | 'n                 | 4.                 | 4.      | ۳.    | 'n                 | ۲.                 | ~                  | ۲.                | ۲.                 | ٦.                |
| *         | Query<br>Match        | 16                 | 16     | 16      | 15     | 15     | 15     | 15     | 12   | 15     | 15               | 14                | 14                | 14     | 14                 | 14                | 13               | 13                 | 13                 | 13                 | 13                 | 13                 | 13      | 13    | 13                 | 13                 | 13                 | 13                | 13                 | 13                |
|           | Score                 | 182                | 8.5    | 177     | 174.5  | 5.5    | 174    | 174    | 174  | _      | .5               | 3.5               | 3.5               | 3.5    | 154.5              | 153.5             | 52               | 9.5                | 149                | 148.5              | 148                | 5.                 | 147     | 5.5   | 146                | 3.                 | 145                | ĸ,                | 5                  | 5.                |
|           | Scc                   |                    | 178    | _       | 174    | 174    | _      |        | -    | _      | 170              | 158               | 158               | 158    | 154                | 153               | -                | 149                | -                  | 148                | -                  | 147.5              | -       | 146.5 | -                  | 145                | ٦                  | 144               | 144                | 144               |
|           | Result<br>No.         | н                  | 7      | М       | 4      | ហ      | 9      | 7      | 80   | σ      | 10               | 11                | 12                | 13     | 14                 | 15                | 16               | 17                 | 18                 | 19                 | 50                 | 21                 | 22      | 23    | 24                 | 25                 | 26                 | 27                | 28                 | 29                |

| coagulation factor       | hypotherical prote | bitiscetin alpha c | phospholipase-A(2) | IgB Fc receptor, 1 | lectin BRA3-2 prec | L-selectin precurs | pulmonary surfacta | pulmonary surfacta | pulmonary surfacta | lectin precursor - | coagulation factor | tetranectin precur | hypothetical prote | IgE Fc receptor II |
|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| JC4329<br>A32375         | T26655             | JC5058             | S48719             | LNMSER             | LNRC3              | S22124             | LINHUPS            | LNHUP6             | LNHUP1             | CNFHLS             | JC4690             | JC4031             | T29200             | S34198             |
|                          |                    |                    |                    |                    |                    |                    |                    |                    |                    | _                  | -                  |                    |                    |                    |
| ~ -                      | 1 (7               | ~                  | 7                  | -                  | ч                  | ~                  |                    | -                  | -                  | -                  | ~                  | ~                  | 'n                 | -                  |
| 372 1                    | 463 2              | 131 2              | 1487 2             | 331 1              | 162 1              | 370 2              | 248 1              | 248 1              | 248 1              | -                  | ~                  | 202 2              | 280 2              | 309 1              |
| 13.0 129 2<br>13.0 372 1 |                    |                    | _                  |                    |                    |                    |                    |                    |                    | 283 1              | 152 2              |                    |                    |                    |
|                          | 13.0               | 13.0               | 12.9               | 12.9               | 12.8               | 12.7               | 12.6               | 12.6               | 12.6               | 12.6 283 1         | 12.6 152 2         | 12.6               | 12.5               | 12.5               |

## ALIGNMENTS

```
mannose receptor precursor - human (5/species: Homo sapiens (man) ```

Assetue: nucleic acid sequence not shown
Assetue: nucleic acid sequence not shown
As Molecule type: mRNA
As Molecule type: mls the nucleotide sequence is incomplete
As Molecule translation of the nucleotide sequence is incomplete
As Molecule translation of the nucleotide sequence is incomplete
As Molecule translation of the gene encoding the human macrophage mannose receptor (MRCI)
As Molecule translation of the gene encoding the human macrophage mannose receptor (MRCI)
As Molecule translation of the gene encoding the human macrophage mannose receptor (MRCI)
As Molecule translation translation of the gene encoding the human macrophage mannose receptor (MRCI)

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translatus: preliminary; nucleic acid sequence not shown; not compared with conceptual translational translationary; Nash, 238-281; 482-569; 631-714, 716-719; 783-820, NV, 822-865, A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:11842

Gaps 54; Query Match
16.5%; Score 182; DB 1; Length 1456;
Best Local Similarity 25.5%; Pred. No. 8.2e-08;
Matches 52; Conservative 37; Mismatches 61; Indels S4

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```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1268 cRNA
A;Cross-references: ENBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g758630
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; E
F;7176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: BGF homology <BGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
F;1167-1123/Domain: complement factor H repeat homology <PHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       versican precursor, splice form V2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14274
R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
B;Schmalfeldt, M.; Dours-zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine bra
A;Reference number: 217954; MUID:98288320; PMID:9624174
                                                                                                                                                                                                                                                           neurocan - mouse
C;Specias: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: S52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
A;Description: Amino acid sequence of mouse neurocan and brevican and their different A;Reference number: S52781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;2-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1097 IGLNDRTVERD------FQWTDNTGLQYENWREKQPDNFFAGGEDCVVWVAHESG--- 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRMP
A;Residues: 1-1643 <SCH>
A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.1%; Score 177; DB 2; Length 1269; Best Local Similarity 31.5%; Pred. No. 1.9e-07; Matches 45; Conservative 17; Mismatches 49; Indels 3.
                                    ------EDAKKTFKESREAALNL 201
                                                                      -----RWNDVPCNYNLPYVCK 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 IGGPYMFQWNDDRCNMKNNFICK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S52781
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Best Local Si
Matches 59,
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A, Status: preliminary
A, Status: 1302, WW, 303-1117, 'E', 1119-1455 < HA2>
A, Cross-references: EMBL: Z11974; NID: 952997; PIDN: CAA78028.1; PID: 952998
R, Hartis, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Super
B, Gochem: Biophys: Res. Commun. 198, 682-692, 1994
A, Title: The exon-intron structure and chromosomal localization of the mouse macrophage
A, Reference number: PC2245; MUID: 94128116; PMID: 8297379
A, Reference number: PC245; MUID: 94128116; PMID: 8297379
A, Residues: 35-105 < HA3>
C, Generics:
A, Gene: Mrc.1
A, Map position: 2
C, Superfamily: phospholipase A2 receptor; C-type lectin homology (2F9)
F, 168-209/Domain: fibronectin type II repeat homology < LCH1>
F, 943-1077/Domain: C-type lectin homology < LCH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mainose receptor precursor, macrophage - mouse
C;Gpecies: Mus musculus (house mouse)
C;Gpecies: Mus musculus (house mouse)
C;Gpecies: Mus musculus (house mouse)
C;Accession: 448925; $21320; $72245
C;Accession: 488925; $21320; $72245
Blood 80, 2363-2373, 1992
A;Title: Characterization of the murine macrophage mannose receptor: demonstration that A;Title: Characterization of the murine macrophage mannose receptor: demonstration that A;Accession: A48925; MUID: 93043353; PMID: 1421407
A;Accession: A48925
A;Accession: A88925
A;Accession: A88925
A;Accession: Muscompared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1455 - 4AR>
A;Residues: 1-1455 - 4AR>
A;Residues: 1-1455 - 4AR>
A;Accession: Muscompared from NUBI backbone (NCBIP: 118733)
B;Harris, N.: Super, M.: Rits, M.: Chang, G; Ezekowitz, R.B.
Submitted to the EMBL Data Library, April 1992
A;Description: Characterization of the murine macrophage mannose receptor: Demonstration
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78 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 135
                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                     ----TMPSVPSGCKEGWNFYSN 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---WNDINCGYPNNFICQRHNSSINATAMP------TTPTTPGGCKEGWHLYKNK 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR 77
                                                                                                                                  136 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      865 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1455;
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Best Local Similarity 25.9%; Pred. No. 1.7e-07;
Matches 53; Conservative 33; Mismatches 66
                                                                                                                                                                                                                                                                                     ---WNDINCGYPNAFICORHNSSINATTVMP-
                                                                                                                                                                                                                                                                                                                                                                                          |::|:|:|:|
955 KCFKIFGFMEEERKNWQEARKACI 978
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                                 807
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	circy actual thought in Bullate proteogram; grycoprotein
Qy 129 AGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGE 169 Db 2277	A./Krobs.references: EMBL:M97161; NID:9205649; PIDN:AAC37679.1; PID:9205650 C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology: Ed
2227 WIGLNDKMFEHDFRWIDGSALQYENWRPNQFDSFFSAGEDCVVI	A; MCCESBIOI: 528/64 A; MCCESBIOI: 528/64 A; Doction of 1970: MRMA
Qy 73 WIGLRRREEKQSNSTACQDLYAWTDGSISGFRNWYVDEPSCGSEVCVVMYHQPSAP 128	A:Ittle: Cloning and primary structure of neurocan, a developmentally regulated, aggrega A:Reference number: S28764; MUID:92406907; PMID:1326557
Db 2179 QGQCYKYPAHRTWDAAERECRLQGAHLTSILSHEEQMFVNRVGHDYQ 2226	R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K. J. Biol. Chem. 267, 19536-19547, 1992
-8	C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 C;Accession: S28764
Best Local Similarity 28.5%; Pred. No. 7.5e-07; Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;	neurocan precursor - rat C;Species: Rattus norvegicus (Norway rat)
Query Match 15.8%; Score 174; DB 1; Length 2397;	RESULT 6 S28764
F;2133-2164/Domain: EGF homology <eg2> F;2171-2291/Domain: C-type lectin homology <lch> F;2298-2354/Domain: complement factor H repeat homology <fhd></fhd></lch></eg2>	Db 3311 KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYPKNSSSAKDN 3361
F;265-346/Domain: link protein repeat homology <lnk2> F;2095-2126/Domain: EGF homology <eg1></eg1></lnk2>	QY 170ETELTTPULPEETQEEDAKKTFKESREAALN 200
F:21-1654/Domain: versican #status predicted <ami> F:21-1654/Domain: versican #status predicted <ami> F:167-244/Domain: link protein repeat homology <lnk1></lnk1></ami></ami>	KPRYEINSLIRYHC
C.Superfamily: versican; C-type lectin homology; complement factor H repeat homology; E	
	DD 3210 WIGHNDKMFEHDFRWHDGSISGERNWXDEPSCGSEVCVWMYHQPSAP 128
A:ACCESSION: ASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	3162
J. B101. Chem. 270, 958-965, 1995 A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generat	OY 14 QRPCYKVIYFHDTSRLNFEBAKBACRRDGGLVSIESEDEGKLIEKFIENLLPSDGDF- 72
C;Accession: A55535 R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.	nes 59; Conserva
C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	Query Match 15.9%; Score 174.5; DB 2; Length 3381;
	Fiz1-3301/Froduct: Versican, Splice form VO #status predicted <mat> F:57,331,352,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2290,2356,26</mat>
versican precursor - mouse N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan	C. Neywolds: Chondrollin Bullate protegglycan; extracellular matrix; glycoprotein F;1-20/Domain: signal sequence #status predicted <51G> F;21-3181/Product: vargical and ice form WA discussion and ice for for form WA discussion and washington and washingt
RESULT 7 A55535	A;Cross-references: EMBL:AF060456; NID:g3253299; PID:g3253300; PIDN:AAC24358.1 C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
Db 1135RWNDVPCNYNLPYVĆK 1150	A;Secures: pterimmiary; cranslated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Reaidues: 1-3381 <sch></sch>
Qy 131 IGGPYMFQWNDDRCNMKNNFICK 153	
1086 IGLNDRIVERDFQWTDNTGLQYENWREKQPDNFFAGGEDCVVWVAHENG	K;SChmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. J. Biol. Chem. 273, 15758-15764, 1998 A;Title: Versican V2 18 a major extracellular matrix component of the mature howine brail
74 TGLBBBBBB	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000 C;Accession: T42389
	Versican precursor, splice form VO - bovine N;Alternate names: chondroitin sulfate proteoglycan C;Species: Bos primigenius taurus (cattle)
Local Similarity 30.8%; nes 44; Conservative 18	RESULT 5 T42389
Query Match 15.8%; Score 174; DB 2; Length 1257;	
F:372.410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted F:944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental	1
F;1156-1212/Domain: complement factor H repeat homology <fhd> F;121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted</fhd>	NDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYE1
F.953-984/Domain: EGF homology vEGF. F.1029-1149/Domain: C-tvne lectin homology <1.775	129 AGIGGPYM
Fil/6-223/Domain: link protein repeat homology <lnk1> Fil/6-255/Domain: link protein repeat homology <lnk2> Fil/6-265/Domain: link protein repeat homology <lnk2></lnk2></lnk2></lnk1>	STLQYENWRPNQPDSFFSTGEDCVV
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mouse
hondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
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A55535; MUID:95122551; PMID:7822336
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ican; C-type lectin homology; complement factor H repeat homology; E
al Sequence #status predicted <SIG>
ersican #status predicted <MAT>
ink protein repeat homology <LNK1>
ink protein repeat homology <LNK2>
BGF homology <EG1>
EGF homology <EG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 72
                                                                                                                                  #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-type lectin homology <LCH>
complement factor H repeat homology <FHD>
                                                                                                                                                                                         i, T.; Zako, M.; Ujita, M.; Kimata, K.
958-965, 1995
                                                                                                                                                                                                                                                                                                                                    y; translated from GB/EMBL/DDBJ
                                                                           raluronate-binding protein
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P:1-29/Domain. girmal gamianca #otatus uradintad .CTC.

Gaps

40;

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chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed durin
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A.Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A.Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A.Experimental source: stage 22-23 developing limb buds
A.Rote: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C.Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lective F;166-243/Domain: link protein repeat homology <LMK1>
F:264-345/Domain: link protein repeat homology <LNK2>
F;3289-3289/Domain: EGF homology <EGF>
F;3256-3327/Domain: EGF homology <EGF>
F;3256-3327/Domain: EGF-Monology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2190 QGQCYK--YF---AHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRV-----GHDYQ 2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2238 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3342 QGQCYK--YF---AHRRTWDTAERECRLQGAHLTSILSHEEQVFVNRI-----GHDYQ 3389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 QRPCYKVIYFHDTSRRLNFEBAKBACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIBSEDEQKLIEKFIENLLPSDGDF-
F;265-346/Domain: link protein repeat homology <LNK2>
F;559-164/Domain: chondroitin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2104-2175/Domain: EGF homology <EG2>
F;2184-2275/Domain: C-type lectin homology <LCH>
F;2180-2302/Domain: C-type lectin homology <LCH>
F;2180-2305/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                         15.8%; Score 174; DB 1; Length 2409; 28.5%; Pred. No. 7.5e.07; tive 23; Mismatches 55; Indels 44
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.5%
Matches 47; Conservative
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A; Molecule type: nucleic acid
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AjkGreenene number: A60979; MUID:8922983; PMID:2469524
AjkGreenelen number: A60979 AjkOreule rype: protein
AjkBreidene (27, Lane, W. S.; Andrews, D.; Dahl, D.; Bignami, A.
AjkGreeniene: 264, 5981-5987, 1989
Ajritie: 1901-2016 and partial characterization of a glial hyaluronate-binding protein.
AjkGreenien unber: A30358; MUID:89174663; PMID:2466833
AjkGreenien number: A30358; MUID:89174663; PMID:2466833
AjkGreenien number: A30358; MUID:89174663; PMID:2466833
AjkGreenien number: A30358; MUID:89174663; PMID:2820959, IR; j261-268;277-283, G', 285-8; Mille: AjkDroblast Chondroitin sulfate proteoglycan core protein contains lectin-like
AjkGreenien number: A20348; MUID:88007514; PMID:2820964
AjkGreenien number: A20348; MUID:99054750; PMID:1429726
AjkGreenien number: A45131; MUID:99054750; PMID:1429726
AjkGreenien number: A55131; MUID:99054750; PMID:1478664
AjkGreeni
                                                                                                                                                    NyAlternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan NyAlternate names: chondroitin sulfate proteoglycan Cispecias: Home sapiens (man)
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Cispecias: Malitiple domains of the large fibroblast proteoglycan, versican.
A;Reference number: Sofolia (mus) 90059882; PMID:2583089
A;Arcession: Sofolia (mus) 90059882; PMID:2583089
A;Accession: Sofolia (mus) 90059882; PMID:2583089
A;Arcession: Sofolia (mus) 90059882; PMID:2583089
A;Cross-references: GB:XI5998; NID:G37662; PIDN:CAA34128.1; PID:G37663
A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by A;Reference number: S43921; MUID:95005762; PMID:7921538
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A;Molecule type: mRNA
A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Residues: 208-440;1094-1385;1910-2246 <YAO>
B;Residues: 208-440;1094-1385;1910-2246 <YAO>
B;Residues: 208-440;1094-1389; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A;Title: Structural similarity of hyaluromate binding proteins in brain and cartilage.
A;Reference number: A60979; MUID:89229983; PMID:2469524
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A;Map position: 5q12-5q14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology;
F;1-20/Domain: signal sequence #status predicted *SIG>
F;21-2409/Product: proteogly/can 24K core protein #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>
                                                                                                                                  versican precursor - human
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8

Gapa

40;

us-09-887-855-2_copy_25_227.rpr

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A.Molecule type: protein
A.Residues: 1230-1249 <-PE2>
A.Residues: 1230-1249 <-PE2>
C.Superfamily: aggreean; C-type lectin homology; complement factor H repeat homology; C.Reywords: glycoprotein
F.89-28/Domain: link protein repeat homology (fragment) <LNK1>
F.89-146/Domain: link protein repeat homology (fragment) <LNK2>
F.80-146/Domain: link protein repeat homology (fragments) <LNK3>
F.167-248/Domain: link protein repeat homology <LNK4>
F.1130-1250/Domain: C-type lectin homology <LCH>
F.1130-1250/Domain: C-type lectin homology <-FHD>
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R;Hering, T.M.; Kollar, J.; Huynh, T.D.
submitred to the EMBL Data Library, September 1996
A;Description: Complete coding sequence of bovine aggrecan: comparative structural and A;Reference number: 222182
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A;Residues: 1-2327 <HER>
A;Cross-references: EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB38524.1
A;Cross-references: EMBL:U76615; NID:g1730259; Complement all source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; C;Reywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggrecan precursor, cartilage long splice form [validated] - human N.Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; N.Contains: aggregating cartilage short splice form C.Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2165 NN---NAQDYQWIGL------NDKTIEGDFRWSDGHSLQFRWRPNQFDNFFATGEDC 2213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 BNLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
C;Accession: 742630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                   A;Reference number: A91327; MUID:85027710; PMID:6489519
A;Accession: E29164
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Pred. No. 9.1e-06;
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A;Molecule type: mRNA
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y 26.8%; Pred. No. 5...
'''e 29; Mismatches
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Best Local Similarity 26.8*
Matches 48; Conservative
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Best Local Similarity 26.8*
Matches 48; Conservative
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C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
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A;Molecule type: protein
A;Rolecule type: protein
A;Resin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomed
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N;Alternate names: aggrecan; aggregating cartilage proteoglycan
C;Species Bos primigenius taurus (cattle)
C;Date: 20-Mar-1992 #sequence revision 23-Mar-1995 #text change 13-Aug-1999
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; D27751; E27751; F27 R;Antonsson, P; Heinegard, D; Oldberg, A.
J; Biol. Chem. 264, 16170-16173, 1989
A;Title: The Keratan sulfate-enriched region of bovine cartilage proteoglycan consists of A;Reference number: A34234; MUID:89380219; PMID:2528543
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: 1-28;59-82;131-137,'QSPT',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
B;Perin, J.P. Bonnet, F.; Jolles, P.
FBBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
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A;Residues: 128-621 <ANT>
A;Cross-references: G8:J05028
R;Oldberg, A: Antonsson, P: Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from
A;Reference number: A2752; MUID:87270630; PMID:3111460
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 622-1340 <0LLD>
B;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by A;Reference number: A39808; MUID:91217051; PMID:2022637
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APPLICANT: Immunex Corporation
APPLICANT: Anderson, Dirk M
TITLE OF INVENTION: LETETIN SS3939 DNA AND POLYPEPTIDES
FILE REFERENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 3.3e-103;
ive 0; Mismatches 0;
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US-09-904-689-137

US-09-904-786-137

US-09-904-786-137

US-09-906-706-137

US-09-906-706-137

US-09-906-706-137

US-09-903-786-137

US-09-903-786-137

US-09-904-139-137

US-09-907-794-137

US-09-907-794-137

US-09-907-925-137

US-09-907-925-137

US-09-905-81-137

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; TYPE: PRT
; ORGANISM: Homo sapiens
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Compugen Ltd.
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Listing first 45 summaries
                                                  protein search, using sw model
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85 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV 144
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                                                                                                                                                                                                                                                                                                                                          25 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFBEAKBACRRDGGQLVSIESEDEQKLIEK 84
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APPLICANT: BURFORD, Nail
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REPERBNCE: PP-0760 PCT
CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT PILLING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR PILING DATE: 1999-12-10; 1999-12-16
SOFTWARE: PERL PROGram
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                                                                                                                                                                                                             Length 374;
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; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1
US-10-149-819-15
                                                                                                                                                                                                                                                              0, Indels
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                                                                                                                                                                                                        Query Match 100.0%; Score 1100; DB 12; Best Local Similarity 100.0%; Pred. No. 7.3e-103; Matches 203; Conservative 0; Mismatches 0;
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100.0%; Score 1100; DB 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-103;
Matches. 203; Conservative 0; Mismatches 0;
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, Sequence 15, Application US/10149819
; Publication No. US20030044913A1
; GENERAL INFORMATION:
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APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: BATTERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
APPLICANT: SHAH, Purvi
APPLICANT: SHAH, Purvi
APPLICANT: ILU, Dyung Aina M.
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2..
SEQ ID NO 2090
LENGTH: 374
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2090
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TYPE: PRT
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APPLICANT: Anderson, Dirk M
TITLE OF INVENTION: LECTIN S33939 DNA AND POLYPEPTIDES
FILE REFERENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEO ID NOS: 9
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1100; DB 9; Best Local Similarity 100.0%; Pred. No. 7.3e-103; Matches 203; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                 Sequence 2, Application US/09887855
Patent No. US20020058310A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: 150GAI, TARAO
APPLICANT: 5UGIYAMA, TOMOYASU
APPLICANT: OTGIXI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: 181HI, SHIZUKO
APPLICANT: 150NO, YUUKO
APPLICANT: 150NO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: HIC, YUKI
APPLICANT: HIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: TOSHIKAWA, TSUTOWU
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US-09-887-855-2
                                                                                                                                                    GENERAL INFORMATION:
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TYPE: PRT
                                                                           US-09-887-855-2
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                        Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                            Gerritsen, Mary E.
                                                                                                                                                                                                                                                                Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                    Kljavin, Ivar J.
Mather, Jennie P.
                        APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                 Desnoyers, Luc
Eaton, Dan L.
                                                                                                                  Fong, Sherman
Gao, Wei-Qiang
US20020132240A1
                                                                                                                                                                      Goddard, A.
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; ORGANISM: Homo sapiens
US-09-909-320-137
                           145 MYHQPSAPAGIGGPYMFQWDDRCNMKONFICKYSDEKPAVPSREAEGEETELTTPVLPE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVV 120
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAGAHARI, KENJI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 064335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                              ETQEEDAKKTFKESREAALNLAY 203
                                                                            205 ETQEEDAKKTFKESREAALNLAY 227
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                                                                                                                                                   Sequence 2142, Application US/10094749 Publication No. US20030219741A1 GENERAL INFORMATION:
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; Sequence 137, Application US/09909320
                                                                                                                                                                                                    SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.5
Matches 202; Conservative
                                                                                                                                                                                          APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2142
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LENGTH: 374
                                                             181
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APPLICANT:
APPLICANT:
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85 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 RLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 84
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Pred. No. 2e-101;
0; Mismatches 0; Indels 8
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
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PRIOR PLING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Best Local Similarity 96.2%;
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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Eaton, Dan L.
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US-09-909-088B-137
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                                                                                                                                                                                           53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 112
                                                                                                                                                                                                                        CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE 172
                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                   25 RLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKBACRRDGGQLVSIESE 84
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                                                            Gaps
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8
         Length 382;
                                                       Indels
    Score 1086; DB 10;
Pred. No. 2e-101;
0; Mismatches 0;
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APPLICANT: Willians, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-0-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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Sequence 137, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
    Query Match

Best Local Similarity 96.2%;
Matches 203; Conservative
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Roy, Margaret Ann
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Tumas, Daniel
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  Query Match
Best Local Similarity
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumae, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,853

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/65,350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-07

PRIOR PILING
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerber, Hanspeter
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; ORGANISM: Homo Sapien
US-09-902-853-137
APPLICANT: Williams, P. Mickey

FILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REPEBRICE: 10466-4114
PRIOR APPLICATION NUMBER: US/09/905,291A
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/2019
PRIOR PLILNG DATE: 1939-09-16
PRIOR PLILNG DATE: 1939-09-16
PRIOR PLILNG DATE: 1939-10-05
PRIOR PLILNG DATE: 1939-10-05
PRIOR PLILNG DATE: 1939-11-29
PRIOR PLILNG DATE: 1939-11-29
PRIOR PRILING DATE: 1939-11-29
PRIOR PLILNG DATE: 1939-11-29
PRIOR PREDICATION NUMBER: PCT/US99/30095
PRIOR PLILNG DATE: 1939-11-29
PRIOR PREDICATION NUMBER: PCT/US99/30095
PRIOR PREDICATION NUMBER: PCT/US99/30095
PRIOR PREDICATION NUMBER: PCT/US99/30099
PRIOR PREDICATION NUMBER: PCT/US99/30099
PRIOR PREDICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PREDICATION NUMBER: PCT/US99/30099
PRIOR PRIOR PREDICATION NUMBER: PCT/US99/30099
PRIOR PREDICATION NUMBER: PCT/US99/300919
PRIOR PLILING DATE: 2000-0-0-0-
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Pred. No. 2e-101;
0; Mismatches 0; Indels 8
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Publication No. US20020192659A1
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Best Local Similarity 96.2%;
Matches 203; Conservative (
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98.7%; Score 1086; DB 10; Length 382;

Query Match

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53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 112
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2e-101;
ches 0; Indels
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96.2%; Pred. No. 2e-10
live 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR APPLICATION NUMBER: PCT/US99/28131
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-02
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1900-01-05
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
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Best Local Similarity 96.21
Matches 203; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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US-09-907-824-137
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
RIOR APPLICATION NUMBER: PCT/US00/04414
RRIOR FILING DATE: 1090-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-015
PRIOR PLING DATE: 1999-09-015
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
                                                                                                                                                                  53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 112
                                                                                                                                                                                          85 DEQXLIEKFIENLLPSDGDFWIGLRRREEKOSNSTACQDLYAWTDGSISOFRNWYVDEPS 144
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                                                                                                                                                                                                                                                                                   1 RLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 52
                                                                                                    25 RLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 84
    Best Local Similarity 96.2%; Pred. No. 2e-101;
Matches 203; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 173 LTTPVLPEETQEEDAKKTFKESREAALNLAY 203
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 137, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same Polypeptides and CURRENT APPLICATION NUMBER: US/09/904,011

PRIOR PELION DATE: 2000-09-18

PRIOR PELION DATE: 2000-09-18

PRIOR PELION DATE: 1999-07-07

PRIOR PELION UNMBER: US 60/145,098

PRIOR PELION UNMBER: US 60/145,22

PRIOR PELION UNMBER: US 60/146,22

PRIOR PELION UNMBER: US 60/146,22

PRIOR PELION UNMBER: PCT/US99/2094

PRIOR PELION UNMBER: PCT/US99/2094

PRIOR PELION UNMBER: PCT/US99/21990

PRIOR PELION UNMBER: PCT/US99/2194

PRIOR PELION UNMBER: PCT/US99/2814

PRIOR PELION UNMBER: PCT/US99/2814

PRIOR PELION UNMBER: PCT/US99/2814

PRIOR PELICATION NUMBER: PCT/US99/2813

PRIOR PELICATION NUMBER: PCT/US99/28056

PRIOR PELICATION NUMBER: PCT/US99/28056

PRIOR PELICATION NUMBER: PCT/US99/30991

PRIOR PELICATION NUMBER: PCT/US99/30995

PRIOR PELICATION NUMBER: PCT/US99/30999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRWWYVDEPS 144
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98.7%; Score 1086; DB 11; Length
Best Local Similarity 96.2%; Pred. No. 2e-101;
Matches 203; Conservative 0; Mismatches 0; Indels
       Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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; ORGANISM: Homo Sapien
US-09-904-011-137
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Best Local Similarity
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                                           ## APPLICANT: Wood, William, 1.

## TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

## CURRENT APPLICATION NUMBER: US/09/907,841

## CURRENT FILING DATE: 2001-11-20

## RIOR APPLICATION NUMBER: US 60/143,048

## RIOR FILING DATE: 1999-07-26

## RIOR FILING DATE: 1999-07-28

## RIOR FILING DATE: 1999-07-28

## RIOR FILING DATE: 1999-09-13

## RIOR FILING DATE: 1999-09-15

## RIOR FILING DATE: 1999-10-05

## RIOR FILING DATE: 1999-10-05

## RIOR FILING DATE: 1999-11-29

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98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 2e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8
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p. US20030003530A1
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US-09-904-011-137
'Sequence 137, Applica.'
'PUBLication No. US2003000.'
'GENERAL INFORMATION:
'PLICANT: Genentech, Inc.'
'PLICANT: Genentech, Inc.'
'PLICANT: Abkenazi, Avi
'CANT: Desnoyers, Luc
'Result Control
'T: Desnoyers, Luc
'Retein, David
'T: Desnoyers, Luc
'T: Tarara, Napole'
'Trara, Napole'
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Williams, P. Mickey Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 96.2
Matches 203; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                                                                                                                          LENGTH: 382
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CGSEVCVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE 172
                        145 CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                173 LTTPVLPEETQEEDAKKTFKESREAALNLAY 203
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CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US/65,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-22

PRIOR PAPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
                                                                                                                                                                                                                            Sequence 137, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT:
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53 DEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 2e-101;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   DB 11;
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 137, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Bllen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
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Hillan, Kenneth, J
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96.2%;
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Paoni, Nicholas F.
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Mather, Jennie P.
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25 RLLSASDLDLRGGQPVCRGGTQRPCXRVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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98.7%; Score 1086; DB 11; Length 382;
Best Local Similarity 96.2%; Pred. No. 2e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1046-14

CURRENT APPLICATION NUMBER: US/09/907,613

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PLING DATE: 2000-02-22

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

PRIOR PLING DA
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
                                           Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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          Filvaroff, Ellen
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                                                                                                                                                                                 Goddard, A.
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; ORGANISM: Homo sapiens
US-09-907-613-137
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETE 172
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                                                      PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
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PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1990-12-07
APPLICATION NUMBER: PCT/US00/04414
FILING DATE: 2000-02-22
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Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Best Local Similarity 96.2%;
Matches 203; Conservative C
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; LENGTH: 382
; TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-137
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US-09-907-613-137
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us-09-887-855-2_copy_24_27.rsp

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December 22, 2003, 16:05:09 ; Search time 6.4979 Seconds (without alignments) 1476.391 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-887-855-2_COPY_24_227 1106 1 GRLLSGQPVCRGGTQRPCYK......EEDAKKTFKESREAALNLAY 204 Title: Perfect score:

Sequence:

127863 segs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	mus musculu	homo sapien	P22897 homo sapien	พนธา		_					Q90953 gailus gali					_	_		_	homo	homod	ម្ហា		-	Q9ygpl trimeresuru	955068 rattus norv	P17346 megabalanus		P18337 mus musculu	~		P07439 megabalanus
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SUMMARIES	CHOD_MOUSE	CHOD HUMAN	MANN HUMAN		PGCN HUMAN	PGCV_BOVIN	PGCN RAT	PGCV_RAT	PGCV MOUSE	DOCT OUT OF	CD93 PAT	PGCA_BOVIN	PGCA_HIMAN	PGCA_CANFA	LEM2 MOUSE	CD93_MOUSE	PGCA_RAT	PGCB_BOVIN	CD93_HUMAN	CLF1_HUMAN	FCE2_HUMAN	PGCA_MOUSE	PGCB_MOUSE	PGCA_CHICK	LECG_TRIST	PGCB_RAT	LEC2_MEGRO	LEM1_RAT	LEM1_MOUSE		LEM2 KAT	LEC3_MEGRO
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Score	574	561.5	182	177	176	2.4.1	174	174	7 7 7	171	165	158.5	158,5	155.5	154.5	153.5	153.5	152	151.5	151	149	147.5	147	146	145	-	144.5	144.5	143.5	141.5	141.0	140.5
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ALIGNMENTS

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TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                    62 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 116
                                                                                                                                                                                                                                                                23 RVVSGQKVCFADVKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES 82
                                                                                                                                                                                                                                                    2 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori M., Fujiyama A., Taylor T.D., Watenabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechechmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawaeki K., Ashtonarakis S., Shincani A., Sasaki T., Nagamine K., Mitsuyama S., Sahtonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weng L., Smits P., Wauters J., Merregaert J.;
Molecular cloning and characterization of human chondrolectin, a
novel type I transmembrane protein homologous to C-type lectins.";
Genomics 80:62-70(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOD HUMAN STANDARD; PRT; 273 AA. 09H972; O9HCY3; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Chondrolectin precursor (Transmembrane protein MT75) (PRED12
                                                                                                                                                                                                          51.9%; Score 574; DB 1; Length 273; 57.4%; Pred. No. 4e-44; iive 26; Mismatches 41; Indels
                                                                                                 CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
N-LINKED (GLCNAC. . .) (POTE
V -> W (IN REF. 2).
T -> K (IN REF. 2).
                                                                                                                                                                                      273 AA; 30303 MW; E052D933F244F4C7 CRC64;
                                                                                 Signal.
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        HSSP, P22897; IEGG.
MGD; MGI:2179069; Chodl.
InterPro: IPR001304; Lectin_C.
Ffam; PF00059; lectin_c; l.
SMART; SM00034; CLECT; l.
PROSITE; PS00615; C_TYPE_LECTIN_2; l.
Lectin; Transmembrane; Glycoprotein; SignAL.
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MEDLINE=20289799; PubMed=10830953;
EMBL; AK014255; BAB29226.1;
                                                                                                                                                                                                                               Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  197 NQ--PEETHE 204
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CHODL OR C21ORF68
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TRANSMEM
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                                                                                                                                                                                                                 23 RVVSGQVCVCFADFKHPCYKMAYFHBLSSRVSFQEARLACESEGGVLLSLENEAEQKLIES 82
                                                                                                                                                                                Gaps
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MEDLINE=92112893; PubMed=1730714;

Taylor M.E., Bezouska K., Drickamer K.;

"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";

J. Biol. Chem. 267:1719-1726(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
MEDLINE=90124192; PubMed=2373685;
Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;
"Primary structure of the mannose receptor contains multiple motifs
resembling carbohydrate-recognition domains.";
J. Biol. Chem. 265:12156-12162(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.
MEDLINE=20347275; PubMed=10779515;
Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99052405; PubMed=1294118;
Kim S.J., Ruiz N., Bezouska K., Drickamer K.;
"Organization of the gene encoding the human macrophage mannose receptor (MRC1).";
Genomics 14:721-727(1992).
                                                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weis W.I.;
"Structure of a C-type carbohydrate recognition domain from the
macrophage mannose receptor.";
                                                                                                                                                        50.8%; Score 561.5; DB 1; Length 273; 60.1%; Pred. No. 5.3e-43; ive 25; Mismatches 35; Indels 7;
                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen).
                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                              C-TYPE LECTIN.
N-LINKED (GLCNAC. . .) (PC
                                                                                                     CYTOPLASMIC (POTENTIAL).
Pfam; PF00059; lectin c; l.
SMART: SM00034; CLECT; l.
PROSITE; PS00615; C.TYPE LECTIN 1; FALSE_NEG.
PROSITE; PS00615; C.TYPE LECTIN 2; l.
Lectin; Transmembrane; GTycoprotein; Signal.
SIGNAL
CHAIN 22 273 CHONDROLECTIN.
DOMAIN 22 216 EXTRACELLULAR
TRANSMEM 217 237 CHONDROLECTIN.
DOMAIN 238 273 CYTOPLASMIC (POTENT DOMAIN 238 273 C-TYPE LECTIN.
CARBOHYD 86 86 N-LINKED (GLCNAC...
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217 237 PO.
238 273 CY.
35 179 CY.
86 86 N-1.
273 AA; 30431 MW; 1
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ID MANR_HUMAN
AC P22897;
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11. J. Biol. Chem. 275:21539-21548(2000).
12. FUNCTION: MEDIATES THE ENDOCYTOSIS OF GLYCOPROTEINS BY MACROPHAGES, IN SEVERAL RECOGNITION AND UPTAKE PROCESSES.
13. C. SUBCELLULAR LOCATION: Type I membrane protein.
14. SIGELLAMBOUS: CRDS 1-3 HAVE AT MOST VERY WEAK AFFINITY FOR CARBOHYDRATE. CRD 4 SHOWS THE HIGHEST AFFINITY BINDING AND HAS MULTISPECIPICITY FOR A VARIETY OF MONOSACCHARIDES. AT LEAST 3 CRDS CC (4, 5, AND 7) ARE REQUIRED FOR HIGH AFFINITY BINDING AND ENDOCYTOSIS OF MULTIVALENT GLYCOCONJUGATES.
15. SIMILARITY: CONTAINS 8 C-type lectin domain.
16. SIMILARITY: CONTAINS 8 C-type lectin domain.
17. C. -- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.
18. C. -- DATABASE: NAME-ENROW, NOTE-PROW 5:85-89(2001).
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO: GO:0005897; C:integral to plasma membrane; TAS.
GO: GO:000587; F:mannose binding activity; TAS.
GO: GO:0004872; F:mannose binding activity; TAS.
GO: GO:0004872; F:receptor activity; TAS.
GO: GO:0004881; P:receptor activity; TAS.
InterPro; IPR00255; AntifreeZell.
InterPro; IPR00355; AntifreeZell.
InterPro; IPR003052; AntifreeZell.
InterPro; IPR003052; Ricin Blectin.
Ffam; PP00659; lectin C; 8
Pfam; PP00659; lectin C; 8
Pfam; PR0055; Ricin Blectin, 2.
Pfam; PR0055; Ricin Blectin, 2.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR0035; ANTIPREZEII.
PRONTS; PR0035; ANTIPREZEII.
PRONTS; SM0034; CLECT; 8.
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M93194; AAA60389.1;
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MIM; 153618; -.
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PDB; 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
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                                                  909 ---WNDINCGYPNAFICORHNSSINATTVMP-----TMPSVPSGCKEGWNFYSN 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 28:405-410(1995).
-I- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
              137 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----
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-i- SIMILARITY: Contains 2 EGF-like domains.
-i- SIMILARITY: Contains 2 link domains.
-i- SIMILARITY: Contains 1 lectin family domain.
-i- SIMILARITY: Contains 1 Sushi (SCR) domain.
-i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and chromosomal localization of the mouse neurocan gene.";
                                                                                                                                                                                                                                                                                                                         Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3) CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=96039250; PubMed=7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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InterPro; IPR002553; Antifreezell.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001881; EGF 2.
InterPro; IPR001881; EGF 2.
InterPro; IPR00599; EGF like.
InterPro; IPR00599; IG-like.
InterPro; IPR001304; IG-like.
InterPro; IPR001304; Linke.
InterPro; IPR001304; Subi; Subi
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PRINTS; PR00356; ANTIFREEZEII.
ProDom; PD000918; Link; 2.
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HSSP; P00740; IEDM.
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Faessler R.;
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FIBRONECTIN TYPE-II.
C-TYPE LECTIN 1 (LONG FORM).
C-TYPE LECTIN 2 (LONG FORM).
C-TYPE LECTIN 3 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 7 (LONG FORM).
C-TYPE LECTIN 9 (LONG FORM).
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014594; Q9UPK6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroltin sulfate proteoglycan 3).
CSPG3 OR NCAN OR NEUR.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                              Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal. 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches 49; Indels 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1268 AA; 137200 MW; 3014E8E202A2FAEC CRC64;
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LINK 1.
LINK 2.
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SUSHI.
SWART; SM00032; CCP; 1.
SWART; SM0004; CLECT; 1.
SWART; SM000409; IG; 1.
SWART; SM00409; IG; 1.
SWART; SM00449; IG; 1.
SWART; SM00446; LINK; 1.
PROSITE; PS00010; ASX HVDROXIL; 1.
PROSITE; PS00010; C_TYPE_LECTIN_1; 1.
PROSITE; PS00021; EGF 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01241; LINK; 2.
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-----RWNDVPCNYNLPYVCK 1161
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                                                                                                 EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                           48; Indels 32; Gaps
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS0835; IG_LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
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Wakaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthoria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGCV BOVIN STANDARD, PRT, 3381 AA.
P81282, 077609, 077610; 077612;
15-DEC-1998 (Rel. 37, Ceated)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Chondroitin sulfate proteoglycan core protein proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          15.9%; Score 176; DB 1; Length 1321; 31.5%; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                         2EF47F823DB980B8 CRC64;
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                                                                                                                                                                                                                                                                                 (IN REF.
                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1e-07
18; Mismatches
                                                                                                                  C-TYPE LECTIN.
SUSHI.
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-----RWNDVPCNYNLPYVCK 1209
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                                                                                                                                                                                                                                                                                                                                           Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 IsoId=P81282-4; Sequence=VSP_003078, VSP_003081;
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed in the central nervous system, and in a number of mesenchymal and cepithelial tissues; the major isoform v2 is restricted to the central nervous system.

DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 link domains.

SIMILARITY: Contains 2 EGF-like domains.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Subhi (SCR) domain.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                           SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                       mature
                                               "Versican V2 is a major extracellular matrix component of the bovine brain.";
Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Interacts with FBLN1 (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P81282-3; Sequence=VSP_003080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=V0;
IsoId=P81282-1; Sequence=Displayed;
                                                                                                      Biol. Chem. 273:15758-15764(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Link.
Sushi_SCR_CCP.
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EMBL; AF060457; AAC24359.1; -.
EMBL; AF060459; AAC24360.1; -.
EMBL; AF060459; AAC24361.1; -.
PIR; T14274; T14274.
PIR; T42389; T42389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00047; ig; 1.
PF00059; lectin_c; 1.
PF00084; sushi; 1.
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                              .mmermann D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=V1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=V2;
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Gaps

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3162 QQQCYK--YF---AHRRTWDAAERBCRLQGAHLTSILSHEBQMFVNRV-----GHDYQ 3209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3210 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG-- 3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3260 ------OWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 3310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE=94230574; PubMed=7513709;
Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
Margolis R.U., Grumet M.;
Margolis R.U., Grumet M.;
"The neuronal chondroitin sulfate proteoglycan neurocan binds to the neural cell adhesion molecules Ng-CAM/L1/NILE and N-CAM, and inhibits neuronal adhesion and neurite outgrowth.";
J. Cell Biol. 125:66-680(1994).
I- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                             15 ORPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDBQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSED IN KIDNEY, LUNG, LIVER AND MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 4) Lest annotation update)
Neurocan core protein precursor (Chondroltin sulfate proteoglycan 3)
(245 Kba early postnatal core glycoprotein) [Contains: 150 kba adult CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=92460907; PubMed=1326557;
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19536-19547(1992).
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Query Match
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R SMART; SM00034; CLECT; 1.

R SMART; SM000179; EGF CA; 1.

R SMART; SM00469; IG; 1.

R RSOILTE; PS001019; EGF CA; 1.

R PROSITE; PS00101; C_TYPE_LECTIN_1; 1.

R PROSITE; PS01166; C_TYPE_LECTIN_2; 1.

R PROSITE; PS01166; EGF_2; 2.

R PROSITE; PS01187; EGF_2; 1.

R PROSITE; PS01187; EGF_2; 1.

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R PROSITE; PS01181; IG_IKE; 1.

R PROSITE; PS01241; LINK; 2.

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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
SUSHI.
BY SIMILARITY.
-!- PTW: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED COLIGOSACCHARIDES (BY SIMILARITY).

-!- PTW: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL. BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF 1; 3.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01241; LIKE; 1.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
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150 kDa ADULT CORE GLYCOPROTEIN
IG-LIKE V-TYPE.
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SMART; SM00034; CLECT; 1.
SMART; SM00104; CLECT; 1.
SMART; SM00109; EGF_CA; 1.
SMART; SM00445; LINK; 2.
SMART; SM00445; LINK; 2.
PROSITE; PS006110; ASX HYDROXYL; 1.
PROSITE; PS006115; C_TYPE_LECTIN_1; 1.
PROSITE; PS006115; C_TYPE_LECTIN_2; 1.
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InterProj IPR003006; IG_MHC.
InterProj IPR003006; IG_MHC.
InterProj IPR003001 Lectin_C.
InterProj IPR000438; Link.
InterProj IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; IGCIn_C; 1.
Pfam; PF00008; IGCIn_C; 1.
Pfam; PF00008; IGCIn_C; 1.
Pfam; PF00008; IGCIn_C; 1.
Pfam; PF00008; ILINKADDULE.
PRINTS; PR001265; LINKADDULE.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                       HSSP; P00740; IEDM.
InterPro; IPR002353; Antifreezell.
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BY SIMILARITY.

CHOURD (GLCNAC. . .) (POTENTIAL).

BY LINKED (GLCNAC. . .) (POTENTIAL).

BY SIMILARITY.

BY SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%; Score 174; DB 1; Length 1257;
30.8%; Pred. No. 1.4e-07;
ive 18; Mismatches 49; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=98308094; PubMed=9642104;
Milev P., Marcal P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding
proteoglycans in developing brain: aggrecan, versican, neurocan, and
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial)
hyaluronate-binding protein) (GHAP) (Fragments).
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Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
"Proteoglycan expression in the normal rat kidney.";
Nephron 77:461-470(1997).
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958 973 BY SIMILARITY.
1029 1040 BY SIMILARITY.
1057 1149 BY SIMILARITY.
1156 1199 BY SIMILARITY.
1166 1199 BY SIMILARITY.
1181 121 BY SIMILARITY.
1182 122 BY SIMILARITY.
121 121 BY SIMILARITY.
123 139 N-LINKED (GLCNAC. . .) (POTENT)
137 737 N-LINKED (GLCNAC. . .) (POTENT)
138 94 94 O-LINKED (GLCNAC. . .) (POTENT)
140 94 94 O-LINKED (GLCNAC. . .) (POTENT)
151 152 NA. 135544 MY, 992B33DCFA19EB1B CRC64;
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Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
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1135 -----RWNDVPCNYNLPYVCK 1150
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ignal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
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                     STRAIN-Sprague-Daviey; TISSUE-Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
Molecular cloning and characterization of two developmentally regulated genes in rat lung.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: May play a role in intercellular signaling and in the regulation of cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-! SUBCUIT: Interacts with FBLNI (By similarity).
-! SUBCELLULAR LOCATION: Secreted; extracellular matrix.
                                                                                                                                                                                                                                                                                 (By similarity).
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
--- SIMILARITY: Contains 2 link domains.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Sushi (SCR) domain.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                     IsoId=09ERB4-3; Sequence=VSP 003092;
TISSUE SPECIFICITY: In kidney is expressed in the papillary area, but not in glomeruli.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
                                                                                                                                                          Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                IsoId=Q9ERB4-2; Sequence=VSP_003091;
                                                                                                                                                                                          IsoId=09ERB4-1; Sequence=Displayed;
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SWART; SW00032; CCP; 1.
SWART; SW000179; CCP; 1.
SWART; SW000179; EGF CA; 1.
SWART; SW00409; IG; 1.
SWART; SW00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00011; C_TYPE_LECTIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000142; EGF 2.
InterPro; IPR001801; EGF 7.
InterPro; IPR001801; EGF 7.
InterPro; IPR001010; IG-like.
InterPro; IPR001309; IG-like.
InterPro; IPR001309; IG-like.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Link
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF062402, AAC40166.1; --
EMBL, U75306, AAB51125.1; --
EMBL, AF08454; AAD48544.1; --
EMBL, AF072892, AAC26116.1; --
EMBL, AY007691, AAG16631.1; --
HSSP; P01132; 1EPG
 [4]
SEQUENCE OF 2535-2738 FROM N.A.
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF 2, 1.
PROSITE; PS0935; IG LIKE; 1.
PROSITE; PS01241; LINK; 2.
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/FTId=VSP_003092.
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                                                                                                                                                                                                                 GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
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                                                                                                                                                                                                                                                                                                      EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
SUSHI.
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2738 AA; 300004 MW; 12CA626D58BDBC6A CRC64;
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                                                          VERSICAN CORE PROTEIN
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Hyaluronic acid; Alternative aplicing.
SIGNAL 1 20 POTENTIAL
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SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).

SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).

CETRAIN-C57BL/6J; TISSUE-Skin;

MEDIINE-21085660; PubMed=11217851;

Xawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Mondaerts P.,

Brownstein M.J., Bult C., Rashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringawald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

Whyshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashi, P., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          versican.";
J. Biol. Chem. 274:20444-20449(1999).
J. Biol. Chem. 274:20444-20449(1999).
J. FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6;
MEDLINE=95181315; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10400671;
Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
"Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                 PGCV MOUSE STANDARD, PRT; 3358 AA.

062059, Q62058; Q9CUU0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STAINA-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-STAIN-ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM V3).
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                                                                                                                                                        TISSUE SPECIFICITY: V2 is found only in brain.
PUSSUE SPECIFICITY: V2 is found only in brain.

TISSUE SPECIFICITY: V2 is found only in brain.

SUMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 link domains.

SIMILARITY: Contains 2 link domains.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Sushi (SCR) domain.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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GLOSALEHA
(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
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IsoId=Q62059-2; Sequence=VSP_003087, VSP_003088;
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                                                                                      lsoId=Q62059-3; Sequence=VSP_003089;
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InterPro; IPR00185; BGF2.
InterPro; IPR00181; BGF2.
InterPro; IPR001801; BGF2.
InterPro; IPR001801; BGF Tike.
InterPro; IPR001809; IGF Tike.
InterPro; IPR001309; IGT Tike.
InterPro; IPR001304; Lactin C.
InterPro; IPR001304; Lactin C.
InterPro; IPR0001304; Link.
InterPro; IPR001304; Link.
IPR00131; XIINK, 2.
IPR0131; SM0019; EGF CA; 1.
SWART; SM00145; LINKMODULE.
SWART; SM00145; LINK, 2.
IPROSITE; PS0010; ASX HYDROXYL; 1.
SWART; SM00145; LINK; 2.
IPROSITE; PS001186; EGF Z; 1.
IPROSITE; PS001186; EGF Z; 1.
IPROSITE; PS01186; EGF Z; 1.
IPROSITE; PS01187; EGF Z; 1.
IPROSITE; PS011
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EMBL; D32040; BAA06802.1; -.
EMBL; AXO14525; BAB29411.1; -.
HSSP; P01132; 1EPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D16263; BAA03796.1; -. EMBL; D28599; -; NOT ANNOTAT
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TISSUE=Brain;
MEDLINE=95181355; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krusius T., Gehlsen K.R., Ruoslahti E.;
"A fibroblast chondroitin sulfate protesglycan core protein contains
lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                  MEDLINE~90059882; PubMed~2583089;
Zimmermann D.R., Ruoslahti E.;
"Multiple domains of the large fibroblast proteoglycan, versican.";
                                                                  Eukaryota, Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   Naso M.F., Zimmermann D.R., Iozzo R.V.;
Characterization of the complete genomic structure of the human
versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
     (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95105187; PubMed=7806529,
Dours-Zimmermann M.T., Zimmermann D.R.;
Na novel glycosaminoglycan attachment domain identified in two alternative splice variants of human versican.";
J. Biol. Chem. 269:32992-32998(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lemire J.M., Braun K.R., Maurel P., Kaplan B.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 251-347 FROM N.A.
MEDLINE=93122792; PubMed=1478664;
LOZZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999)
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TISSUE-Aortic smooth muscle;
MEDLINE-99327053; PubMed=10397680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Versican/PG-M isoforms in vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 270:3914-3918(1995)
                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM VO).
MEDLINE=95105188; PubMed=7528742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 2711-3396 FROM N.A.
TISSUE-Lung fibroblast;
MEDLINE=88007514; PubMed=2820964;
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MEDLINE=96213482; PubMed=8627343;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM V1).
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                                                                                                                                                                                                                                                                                                                                   EMBO J. 8:2975-2981 (1989)
                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                     tumor;
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                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    TISSUE=Placenta;
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28.5%; Pred. No. 4.8e-07;
ive 23; Mismatches 55; Indels 40; Gaps
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/FTId=VSP 003087.
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P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1997 (Rel. 13, Essentence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
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TVWNSNS -> QFGIQTA (IN REF. 3).
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Isoid=P13611-5; Sequence=VSP_003086;
ISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed in normal brain, gliomas, medulloblastomas, schwannomas, neurofibromas, and menningiomas; v2 is restricted to normal brain and gliomas; v3 is found in all these tissues except medulloblastomas.
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-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 2 link domains.
-1- SIMILARITY: Contains 2 EGF-like domains.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 Sushi (SCR) domain.
-1- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005204; F:chondroitin sulfate proteoglycan; TAS.
GO; GO:000540; F:chondroitin sulfate proteoglycan; TAS.
GO; GO:000540; F:chal recognition; TAS.
GO; GO:0007275; P:cell recognition; TAS.
Interbro; IPR000152; Asx hydroxyl.
Interbro; IPR00184; EGF_2.
Interbro; IPR001881; EGF_2.
Interbro; IPR001801; EGF_1ike.
                                                                                                                                                                                                                                                                                                                                                               IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
                                                                                                                                                                                                                                                                                     IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=5; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                        IsoId=P13611-3; Sequence=VSP_003084;
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InterPro; IPR003006; Ig.MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR0000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
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Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
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3225 WIGL------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3274
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
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VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE.
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ID PGCV CHICK STANDARD; PRT; 3562 AA.

AC Q90953; Q90945;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
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SWART; SMO0022; CCP; 1.
SWART; SMO004; CLBCT; 1.
SWART; SMO019; EGP_CA; 1.
SWART; SMO0409; IG; 1.
SWART; SMO0445; LINK; 2.
PROSITE; PS00110; ASX HYRROXYL; 1.
PROSITE; PS00110; C_TYPE_LECTIN_1; 1.
PROSITE; PS00012; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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LINK 2.
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les 47; Conservative
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                           Gallus gallus (Chicken).
Eukeryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                     Isoid-090953-2; Sequence=VSP_003093;
-1-TISSUE SPECIFICITY: Prechondrogenic condensation area of developing limb buds.
-1- DEVELOPMENTAL STAGE: Disappears after the cartilage development (By similarity).
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 2 link domains.
-1- SIMILARITY: Contains 2 EGF-like domains.
-1- SIMILARITY: Contains 1 EGF-like domains.
-1- SIMILARITY: Contains 1 Sushi (SCR) domain.
Versican core protein precursor (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                     IsoId=Q90953-1; Sequence=Displayed;
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EMBL, D13542; BAA02742.1; --
FIR, A47171; A47171.
HSSP, P00740; 1EDM.
INTERPRO; IPR000152; ABx hydroxyl.
INTERPRO; IPR000742; BGF 2.
INTERPRO; IPR00181; EGF Ca.
INTERPRO; IPR00181; EGF Ca.
INTERPRO; IPR005109; IGF IRE.
INTERPRO; IPR007100; IG-IiRE.
INTERPRO; IPR003100; IG-IIRE.
INTERPRO; IPR0031006; IG-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001304; Lectin C.
InterPro; IPR001398; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00009; EGF, 2.
Pfam; PF00047; ig; 1.
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R Pfam; PF00084; sushi; 1.

Pfam; PF00193; Xlink; 2.

PRINTS; PR01265; LINKMODULE.

ProDom; PD000318; Link; 2.

SMART; SM00032; CCP; 1.
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SM00179; EGF_CA; 1
SM00409; IG; 1.
                                                        Gallus.
NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                           LINK 2.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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28.5%; Pred. No. 9.7e-07;
Live 23; Mismatches 55; Indels 40; Gaps
                                                                                                                                        Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
SIGNAL 1 26 POTENTIAL.
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PROSITE; PSO0010; ASX_HYDROXYL; 1.
PROSITE; PSO0615; C_TYPE_LECTIN 1; 1.
PROSITE; PSO0041; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01181; EGF 2; 1.
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InterPro; IPR001304; Lectin_C.
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SEQUENCE FROM N.A.

STRAIN=wister; TISSUE=Lung;
MEDLINE=20607883; PubMed=1034210;
MEDLINE=20607883; PubMed=1034210;

Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;
Molecular and cellular properties of the rat AA4 antigen, a C-type Tiechin-like receptor with structural homology to thrombomodulin.";

To Biol. Chem. 275:34382-34392(2000).

Cid, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in interaction with soluble defense collagens. May play a role in interactilular adhesion.

CINESTELULAR LOCATION: Type I membrane protein.

CINESTELLIAR LOCATION: Type I membran
3390 WIGL------NDKAPERDFRWIDGSPLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                 ט
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PVG; TISSUE=Natural killer cells; MEDLINE=20545218; PubMed=11093152; Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.; "Characterization and molecular cloning of rat C1qRp, a receptor on NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (see http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Complement component Clg receptor precursor (Complement component L)
subcomponent, receptor 1) (ClgRp) (ClgR(p)) (Clg/MBL/SPA receptor)
(CD93 antigen) (Cell surface antigen AA4).
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                            130 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0016021; C:integral to membrane; ISS. GO:0004872; F:receptor activity; ISS. GO:0016337; P:cell.cell adhesion; ISS. GO:0042116; P:macrophage activation; ISS. GO:0006909; P:phagocytosis; ISS.
                                                                                                                                                                                    643 AA
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells.";
Eur. J. Immunol. 30:3355-3362(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF136537; AAG01572.1; -. EMBL; AF160978; AAF80402.1; -.
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P35555; IEMN.
GO; GO:0016621; C:ir
GO; GO:0004872; F:re
GO; GO:0016337; F:re
GO; GO:0042116; P:mc
GO; GO:0006909; P:pb
                                                                                                                                                                                                                                                                                                                                                                                                                           [1] TSEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                          3440
                                                                                                                                                                                    CD93 RAT
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                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASNIC (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GRLLSGQP-----VCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQKLIEKFIENLL----PSD---GDFWIGLRRREEKQSNSTACQDLYAWT-DGSISQFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WY-VDEPSCGSEVCVVMY-----HQPSAPAGIGGPYMFQWNDDRC------NMKNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 WYKASKSKISKRCVSLILDLSLKPHPSHLP-----KWHESPCGTPDAPGNSIEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGCA BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; Q28159;
01-JAN-1990 (Rel. 13, Created)
01-JOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                 COMPLEMENT COMPONENT C10 RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 643;
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 5.
Pfam; PF00059; lectin c; 1.
SMART; SM00134; CLECT; 1.
SMART; SM00104; CLECT; 1.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS001186; EGF 2; 3.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01187; Receptor; Repeat; Signal; Transmembrane; EGF-like domain; Lectin; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        %; Pred. No. 4e-07;
35; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9AE4C933AD943DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%; Score 165; 25.2%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ICKYSDEKPAVPSREAEGEETELTTP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 25.2 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448888444
448888444
448846444
448846444
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643 AA;
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Contains 1 immunoglobulin-like V-type domain

SIMILARITY: SIMILARITY:

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ISOZIG-P13608-2; Sequence-VSP 003072;
DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTECGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE C-PERMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                           Antonsson P., Heinegaard D., Oldberg A.;
"The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 206:73-77(1986).

-!- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINIAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perin J.-P., Bonnet F., Jolles J., Jolles P.,
"Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligomolectide probe.";
FEBS Lett. 176:37-42(1984).
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan,
deduced from a cDNA clone, contains numerous Ser-Gly sequences
arranged in homologous repeats.";
Biochem. J. 243:255-259(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like
domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE.

***MEDIJIRE=87005253; FubMed=3530809;

***Perin J.P., Bonnet F., Jolles P.;

"Structural relationship between link proteins and proteoglycan
                                                                                                                          SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
ALTERNATIVE PRODUCTS:
Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P13608-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 268:17377-17383(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2114-2150 FROM N.A.
TISSUE-Cartilage;
MEDLINE-93352525; PubMed-8349621;
                                                                                                                                                                                                                             MEDLINE=89380219; PubMed=2528543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85027710; PubMed=6489519;
                                                                                                                                                                                                         SEQUENCE OF 563-1056 FROM N.A.
                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE.
                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monomers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   module.
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PTM: CONTAINS MOSTLY CHONDROITIN SULPATE, BUT ALSO N-LINKED AND O-LINKED ADDOUT 40) OLIGOSACCHARIDES.
PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN ADULT AND PETAL BOVINE PROTEOGLYCANS.

AND G3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         Contains 4 link domains.
Contains 1 EGF-like domain.
Contains 1 C-type lectin family domain.
Contains 1 Sushi (SCR) domain.
BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CS-2.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain; Calcium; Alternative splicing; Repeat; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGRECAN CORE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINK 1.
LINK 2.
LINK 4.
LINK 4.
23 X 6 AA APPROX
E-[EK]-P-F-P-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                  InterPro; IPR006209; EGF_like.
InterPro; IPR001010; IG-like.
InterPro; IPR001010; IG-like.
InterPro; IPR001014; Lectin_C.
InterPro; IPR001314; Link.
InterPro; IPR001314; SGXXSG.
InterPro; IPR001314; SGXXSG.
InterPro; IPR001014; Sushi_SCR_CCP.
Pfam; PF00009; EGF; 1.
Pfam; PF00019; IGF; 1.
Pfam; PF001319; SGXXSG; 61.
Pfam; PF00131; Xlink; 4.
                                                                                                                                                                          EMEL; 107053; -; NOT ANNOTATED CDS. PIR; 742630; 142630; 142630. HSSP; P08709; 18F9. InterPro; IPR001535; Abx hydroxyl. InterPro; IPR001535; Abx hydroxyl. InterPro; IPR001891; EGF 2. InterPro; IPR001881; EGF 2. InterPro; IPR001881; EGF 2. InterPro; IPR001801; EGF 1ike. InterPro; IPR001081; EGF 1ike. InterPro; IPR003006; Ig MHC. InterPro; IPR003006; Ig MHC. InterPro; IPR003006; Ig HHC. InterPro; IPR003006; Ig HHC. InterPro; IPR003006; Ig HHC.
                                                                                                                                                                  EMBL; U76615; AAB38524.1;
EMBL; L07053; -; NOT ANNOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2112
2149
2364
2276
2338
                                SIMILARITY: C
SIMILARITY: C
SIMILARITY: E
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25
170
268
504
602
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2113
2114
2114
2216
2280
2280
175
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199
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DOMAIN
DISULFID
DISULFID
DISULFID
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2202 NN---NAQDYQWIGL------NDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDC 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2251 VVMIWHEKG------EWNDVPCNYQLPFTCKKGTVACGEPPVVEHARIFGOKKD 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGCA HUMAN STANDARD; PRT; 2415 AA.
P16.12; Q13650;
01-APR-1990 (Rel. 14, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2009 (Rel. 92, Last annotation update)
Protein core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
AGCI OR CSPGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 3).
TISSUB=Chondrocytes;
MEDLINE=91093289; PubMed=1985970;
MEDLINE=91093289; PubMed=1985970;
Complete coding sequence and deduced primary structure of the human cartilage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).
MEDLINE=89380154; PubMed=2789216;
Baldwin C.T., Reginato A.M., Prockop D.J.;
"A new epidermal growth factor-like domain in the human core protein for the large cartilage-specific proteoglycan. Evidence for alternative splicing of the domain.";
J. Biol. Chem. 264:15747-15750(1989).
                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 158.5; DB 1; Length 2364; Pred. No. 7.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6FF83763420C3D4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases
BY SIMILARITY.
CLUNED (GLCNAC. ...) (P.
N-LINKED (GLCNAC. ...) (P.
M.BELINGED (GLCNAC. ...) (P.
M.BELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1778-2415 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2364 AA; 246359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
                                                                                                      652
2128
2274
2266
2337
126
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !ISSUE=Chondrocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                           2117
2182
2250
2250
2281
2310
126
239
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     DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                        SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOIG=P16112-3; Sequence=VSP 003074, VSP 003075; DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTECGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. GI CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                         aggrecan.";
Matrix Biol. 14:323-228(1994).

Matrix Biol. 14:323-228(1994).

PUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR HATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.

-!- SUBUNIT: Interacts with FBLN1 (By similarity).

-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                       Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 155760; -.
GO; GO:0005204; F:chondroitin sulfate proteoglycan; TAS.
                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P16112-2; Sequence=VSP_003074;
                                                                                                                                                                                                                                                                                                                                                               IsoId=P16112-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR002353; AntifreezeII.
InterPro, IPR006209; EGF like.
InterPro, IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sushi SCR CCP
                                                   MEDLINE=95128522; PubMed=7827755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003099; Ig.
InterPro; IPR001006; Ig.MC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001314; SGXSG.
InterPro; IPR001314; SGXSG.
                 SEQUENCE OF 764-864 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M55172; AAA62824.1; -.
EMBL; J05062; AAA35726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; JOSO62; AAA35726.1; -. EMBL; X17406; CAA35463.1; -. EMBL; X174659; AAC60643.2; -. PIR; A39086; A39086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin_c; l.
Pfam; PF02339; SGXXSG; 71.
Pfam; PF00084; sushi; l.
Pfam; PF00193; Xlink; 4.
                                                                                                                                                                                                                                                                     similarity).
ALTERNATIVE PRODUCTS:
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                                   TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                             Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3;
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2202 QEVCEBGWNKYQGHCYR--HFPD---RETWVDAERRCREQQSHLSSIVTPEEQ----EFV 2252
                                                                                                                                                                                                                                                64 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 119
                                                                                                                                                                                                                                                                                                 120 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 173
                                                                                                                                                                                                                                                                                                                                                                      PGCA_CANFA STANDARD; PRT; 2333 AA.
028343; 028310;
01-00V-1997 (Rel. 35, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fueloep C.; "Complete coding sequence and deduced amino acid sequence of aggrecan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).

DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTEOGLYCAN, WILLE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE CONTINEMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP SYRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
                                                                                                                                                                               7 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                      Indels 43; Gaps
                                                                                                                           Length 2415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 774-833 FROM N.A.
TISSUB=Cartilage;
MEDLINE=951252; PubMed=7827755;
BARTY F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
                                                                                       2391 A -> P (IN REF. 2 AND 3). '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of canine cartilage.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
NCBI_TaxID=9615;
                                                                                                                           Query Match 14.3%; Score 158.5; DB 1; Best Local Similarity 29.1%; Pred. No. 7.8e-06; Matches 52; Conservative 22; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2082-2118 FROM N.A.
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Matrix Biol. 14:323-328(1994).
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Canis familiaris (Dog)
                                                                                       2391 239
2415 AA;
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G1-B'.

G2-B'.

G2-B'.

I2 X APPROXIMATE TANDEM REPEATS.

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CS-2.

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Missing (in isoform 3) /FIId=VSP_003075.
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E -> V (IN REF. 4).
E -> V (IN REF. 2).
E -> V (IN REF. 2).
T -> V (IN REF. 2 AND.
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AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
LINK 1.
LINK 2.
LINK 3.
LINK 4.
LINK 4.
EINK 4.
EINK 4.
G1-B.
G1-B.
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G1-B.
G2-B.
KS.
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EMBL; G74662; AAC66527.1; -
EMBL; L07054; -; NOT_ANNOTATED_CDS.
HSSP; P087099; 18F9.
InterPro; IPR001152; Aax hydroxyl.
InterPro; IPR001152; Aax hydroxyl.
InterPro; IPR001181; EGF_Ca.
InterPro; IPR00181; IRF.
InterPro; IPR001019; IRF.
InterPro; IPR001304; IRF.
InterPro; IPR001304; ISF.
InterPro; IPR001314; ISF.
INTERPRO; IPR0013144; ISF.
INTERPRO; IPR001446; ISF.
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2171 NN---NAQDYQWIGL------NDRTIEGDFRWSDGHSLQFENWRPNQPDNFFVSGEDC 2219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2220 VVMIWHEKG------EWNDVPCNYYLPFTCKKGTVACGDPPVVEHARTFGQKKD 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKBACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 155.5; DB 1; Length 2333;
; Pred. No. 1.4e-05;
24; Mismatches 61; Indels 43; Gaps
CS-1.
CS-2.
G3-2.
G3-2.
G3-2.
G4 SIMILARITY
BY SIMILARITY

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Best Local Similarity 28.5.,

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 16:06:34 ; Search time 9.91785 Seconds (without alignments) 1978.090 Million cell updates/sec Run on:

US-09-887-855-2_COPY_24_227 1106 1 GRLLSGQPVCRGGTQRPCYK......EEDAKKTFKESREAALNLAY 204 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ES	Description	r rotanger eschass	receptor	4004000-0	_					chondroitin sulfat	mannose receptor.	Droteoglycan core	addrecan - howine	addrecan precursor	E-selectin precura	proteoglycan core	brevican precureor	hypothetical profe	IGE For receptor II		protein F52E1.2 (i	addrecan precursor	brevican precursor	lectin BRA3-1 prec	addrecan precursor	SCavender recentor	brevican precursor	lectin - harnarle	L-selectin predure	HIV gp120-binding
SUMMARIES	QI	A36563	A48925	S52781	T14274	T42389	\$28764	A55535	A60979	A47171	T42710	A39808	T42630	A39086	B42755	A28452	A54423	T24425	LNHUER	T46256	E89130	A55182	S57653	LNRC1	I50421	JC7595	S49126	S10548	\$23936	A46274
	DB	-	Н	7	7	7	ď	Н	- -1	N	~	7	~	7	7	~	~	~	-	N	~	-	7	7	ч	~	~	~	~	0
	Length	1456	1455	1268	1643	3381	1257	2397	2409	3562	1479	1340	2327	2415	612	2124	912	459	321	330	253	2132	883	162	2109	742	883	173	372	404
d	Query Match	16.5	16.1	16.0	15.8	15.8	15.7	15.7	15.7	15.5	15.4	14.3	14.3	4.		13.9	13.7	13.5	13.5	13.4	ຕ	13.3	13.3	13.2	13.2	13.2	13.1	13.1	٠	13.1
	Score	182	178.5	177	174.5	174.5	174	174	174	171	170.5	158.5	158.5	158.5	154.5	153.5	152	149.5	149	148.5	14	147.5	₹8	146.5	14	145.5	145		144.5	144.5
	Result No.	H	7	e	4	ß	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50

coagulation factor	L-selectin precurs	hypothetical prote	bitiscetin alpha c	phospholipase-A(2)	IqE Fc receptor, 1	lectin BRA3-2 prec	L-selectin precurs	pulmonary surfacta	pulmonary surfacta	pulmonary surfacta	lectin precursor -	coaqulation factor	tetranectin precur	hypothetical prote	igk Fc receptor II
JC4329	A32375	T26655	JC5058	S48719	LINMSER	LNRC3	S22124	LNHUPS	LNHUP6	LNHUP1	LNFHLS	JC4690	JC4031	T29200	S34198
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129	372	463	131	1487	331	162	370	248	248	248	283	152	202	280	309
13.0	13.0	13.0	12.9	12.8	12.8	12.7	12.7	12.6	12.6	12.6	12.6	12.5	12.5	12.5	12.4
143.5	143.5	143.5	142.5	142	141.5	140.5	140	139	139	139	139	138.5	138.5	138	137.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C.Species: Homo sapiens (man)
C.Species: No. 89-1999 #eacture crevision 10-Sep-1999 #text change 10-Sep-1999
C.Accession: A36563, A60926, A44355; G44355; D44255; D44255; B44255; P44255; P44255; D44255; D44251
C.Accession: A36563, A60926, A44355; B44355; C44355; D44255; D44255; P4255; D44255; D44251
J. Biol. Chem. 265, 12166-12162, 1990
A.Piclie: Primary Estructure of the mannose receptor contains multiple motifs resembling
A.Reference number: A35663
A.Molecule type: mRNA
A.Resion: A56563
A.Molecule type: mRNA
A.Resion: A60926, MID: 9107319; PMID: 237685
A.Recerence number: A60926, MID: 9107939; PMID: 2258707
A.Recerence number: A60926, MID: 9107939; PMID: 2258707
A.Recession: A60926
A.Recession: A60926, MID: 9107939; PMID: 2258707
A.Recession: A60926, MID: 9107939; PMID: 2258707
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A.Recession: A44255
A.Recession: A44255
A.Recession: A44256
A.R
mannose receptor precursor - human
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54; 16.5%; Score 182; DB 1; Length 1456; 25.5%; Pred. No. 8.8e-08; tive 37; Mismatches 61; Indels 54 Conservative Query Match Best Local Similarity Matches 52; Conserval

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A;Accession: S52781
A;Status: preliminary
A;Status: preliminary
A;Molocule type: mRNA
A;Rollocule type: mRNA
A;Rollocule type: mRNA
A;Rollocule type: mRNA
A;Cross-references: EMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g758630
A;Cross-references: EMBL:X84727; NID:g758629; Complement factor H repeat homology; E
F;274-255/Domain: link protein repeat homology <LNK2>
F;274-355/Domain: EGF homology EGF>
F;1040-1160/Domain: CGF homology EGF>
F;1040-1160/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       versican precursor, splice form V2 - bovine (Species: Bos primigenius taurus (cattle) (Cispecies: Bos primigenius taurus (cattle) (Cispecies: Bos primigenius taurus (cattle) (Cispecies: Do.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000 (Cispecession: T14274 (Cispecies) (Cispe
                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: S52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, Pebruary 1995
A;Description: Amino acid sequence of mouse neurocan and brevican and their different
A;Reference number: S52781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1643 <SCH>
A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 ORPCYKVIYFHDTSRRINFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1048 QCHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Score 177; DB 2; Length 1268; 31.5%; Pred. No. 2.1e-07; ive 17; Mismatches 49; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
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                                                                                         -----RWNDVPCNYNLPYVCK 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 IGGPYMFQWNDDRCNMKNNFICK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Conservative
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Matches 59; Conserv
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A48925; 231320; P62245
Blood 80, 2361-2313, 1992
A;Title: Characterization of the murine macrophage mannose receptor: demonstration that A;Reference number: A48925; MUID:93043353; PMID:1421407
A;Recension: A48925
A;Reterence number: A48925; MUID:93043353; PMID:118733)
A;Reterence number: BNAA
A;Reterence number: peritoneal macrophage
A;Reterence number: S21320
A;Reterence number: S21320
A;Reterence number: S21320
A;Reterence number: S21320
A;Reterence number: BNID:1974; MID:922997; PIDN:CAA78028.1; PID:952998
A;Molecule type: mRNA
A;Reterence number: BNID:11874; MID:922997; PIDN:CAA78028.1; PID:952998
A;Molecule type: mRNA
A;Reterence number: BNID:11074; MID:922997; PIDN:CAA78028.1; PID:952998
A;Molecule type: mRNA
A;Reterence number: Pid: Eicher R.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Super
Biochem: Biophys: Res. Commun. 198, 682-692, 1994
A;Reterence number: PC2245; MUID:94128116; PMID:8297379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     re
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-----TMPSVPSGCKEGWNFYSN 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---WNDINCGYPNNFICQRHNSSINATAMP-----TTPTTPGGCKEGWHLYKNK 953
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                                                                                                                 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY
                                                                                                                                                                       ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY----SNSGF----
                                                                                                                                                                                                                                                             137 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              865 ISMDKK-----TIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1455;
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A, Molecule type: mRNA
A, Residues: 35-105 < HA3>
C, Genetics:
A, Gene: Mrc1
A, Map position: 2
C, Superfamily: phospholipase A2 receptor; C-type lectin hc; Reywords: membrane protein; receptor
F; 168-209/Domain: fibronectin type II repeat homology < 2F; F; 361-465/Domain: C-type lectin homology < LCH1>
F; 943-1077/Domain: C-type lectin homology < LCH2>
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25.9%; Pred. No. 1.8e-07;
:ive 33; Mismatches 66
                                                                                                                                                                                                                                                                                                                               ----WNDINCGYPNAFICQRHNSSINATTVMP---
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Matches 53; Conserv
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F;1-22/Domain: signal sequence #status predicted <sig> F;23-1257/Product: neurocan #status predicted <mat> F;23-1257/Product: neurocan #status predicted <mat> F;176-253/Domain: link protein repeat homology <lnkl> F;274-355/Domain: link protein repeat homology <lnk2> F;364-366/Region: cell attachment (R-G-D) motif F;364-366/Region: cell attachment (R-G-D) motif F;303-984/Domain: EGF homology <egf> F;1050-1149/Domain: C-type lectin homology <lgh> F;1050-1149/Domain: complement factor H repeat homology <fhd> F;1050-1149/Domain: complement factor H repeat homology <fhd> F;102-1149/Domain: complement factor H repeat homology <fhd> F;102-1149/Domain: complement factor H repeat homology <fhd> F;103-1149/Domain: GMF homology in suffactor H repeat homology of the status predicted F;342,410/Binding site: chondroltin sulfate (Ser) (covalent) #status predicted F;344/Binding site: chondroltin sulfate (Ser) (covalent) #status experimental Query Match Query Match Query Match At; Score 174; Score 174; Score 174; Score 175; Best Local Similarity 30.8%; Pred. No. 3.8e-07; Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6; Qy 15 QRPCYKVIYFHDTSRRINFEBAKEACRREGGOLVSIESEDEOKLIEKFIENLIPSEDEPW 74</fhd></fhd></fhd></fhd></lgh></egf></lnk2></lnkl></mat></mat></sig>	Db 1037 QGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSFGHENSW 1085 QY 75 IGLRRREEKQSNSTACQDLVAWTDGSISQFRNWTVDEPSCGSEVCVWYTQPSAPAG 131 Db 1086 IGLNDRTVERDFQWTDNTGLQYENWREKQPDNFFAGGEDCVVWYAHENG1134 QY 132 IGGPYWFQWNDDRCNWRNNFICK 154 Db 1135RWNDVPCNYNLPYVCK 1150 RESULT 7 AS5535 Versican precursor - mouse	N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan versican versi	C;Superfamily: versical, C-try, mr. 9001099; complement factor H repeat homology; F F1-20/Domain: signal sequence #status predicted <sig> F1-20/Domain: signal sequence #status predicted <sig> F21-1654/Domain: versical #status predicted <mat> F21-1654/Domain: versical #status predicted <mat> F167-244/Domain: ink protein repeat homology <lnk1> F265-346/Domain: link protein repeat homology <lnk2> F2095-2126/Domain: EGF homology <eg1> F2133-2164/Domain: EGF homology <eg1> F2133-2164/Domain: EGP homology <eg1> F2133-2164/Domain: G-type lectin homology <lch> F2296-2354/Domain: C-type lectin homology <eg1> F2296-2354/Domain: Complement factor H repeat homology <fhd></fhd></eg1></lch></eg1></eg1></eg1></lnk2></lnk1></mat></mat></sig></sig>	Query Match Best Local Similarity 28.5%; Score 174; DB 1; Length 2397; Best Local Similarity 28.5%; Pred. No. 8e-07; Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8; Qy 15 QRCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-73 Db 2179 QGQCYKYPAHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRVGHDYQ 2226 Qy 74 WIGLRRREKQSNSTACQDLYAWTDGS1SQFRNWYVDEPSCGSEVCVVMYHQPSAP 129 Db 2227 WIGLNDKMFEHDFRWTDGSALQYENWRPNQPDSFFSAGEDCVVIIWHENG 2276 Qy 130 AGIGGPYMFQWNDDRCNWKNNFICKYSDEKPAVPSREAGE 170 Db 2277QWNDVPCNYHLTYTCKKGTVACGOPPVVENAKTFGK 2312
Qy 74 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYUDEPSCGSEVCVWYHQPSAP 129 Db 1472 WIGLNDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSTGEDCVVINHENG 1521 Qy 130 AGIGGPYMFQWNDDRCNMKGNFICKYSDEKPAVPSREAGGE	chondroitin sulfate proteoglycan igenius taurus (cattle) #sequence_travision 03-Dec-1999 #text_change 05-May-2000 Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. 15758-1576-1576-1992 #text_component of the mature bovir 217954; MUID:98288320; PMID:9624174 Ky; translated from GB/EMBL/DDBJ AAACA4158.1 SCHA. SCHA. ACCA4158.1 SCHA. ACCA4158.1 SCHA. ACCA4158.1 SCHA. ACCA4158.1 CHA. ACCA4158.1 SCHA. ACCA4158.1 CHA. ACCA4158.1 SCHA. ACCA4158.1 CHA. ACCA4158.1	### sequence ### seatus predicted <pre>sequence ### seatus predicted <pre>c</pre></pre>	170 3310	RESULT 6 S28764 neurocan precursor - rat C;Species: Rattus norvegicus (Norway rat) neurocan precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 S28764 S;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K. J; Biol. Chem. 267, 19536-19547, 1992 A;Reference number: S28764; MUID:92466907; PMID:1326557 A;Accession: S28764 A;Molecule type: mRNA A;Residues: 1-1257 - RAU> A;Residues: 1-1257 - RAU> A;Cross-references: EMBL:M97161; NID:9205649; PIDN:AAC37679.1; PID:9205650 C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG C;Keywords: chondroitin sulfate proteoglycan; glycoprotein

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C,Accession: A47171
R,Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A,Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed durin
                                                                                                                                                                                                                                                                                                                                                                                                                      2190 QGQCYK--YF---AHRRTWDBAERECRLQGAHLTSILSHEEQMFVNRV-----GHDYQ 2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2238 WIGL------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3342 QGQCYK--YF---AHRRTWDTAERECRLQGAHLTSILSHEEQVFVNRI-----GHDYQ 3389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3390 WIGL------NDKOMFERDFRWIDGSPLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 129
                                                                                                                                                                                                                                                                                                                                                                               15 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 WIGLRRREEKOSNSTACODLYAWIDGSISOFRNWYVDEP----SCGSEVCVVMYHQPSAP 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 21-Jul-2000
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N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: nucleic acid
A; Residues: 1-3562 <SHI>
A; Residues: 1-3562 <SHI>
A; Residues: 1-3562 <SHI>
A; Residues: 1-3562 <SHI>
A; Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A; Experimental source: stage 22-23 developing limb buds
A; Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457
C; Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein
F; 166-243/Domain: link protein repeat homology <LNKI>
F; 264-345/Domain: link protein repeat homology <LNKI>
F;265-346/Domain: link protein repeat homology <LNK2>
P;559-1654/Domain: chondroitin sulfate attachment #status predicted P;2106-2137/Domain: EGP homology <EG1>
P;2144-2137/Domain: EGF homology <EG2>
P;2184-2137/Domain: C-type lectin homology <LCH>
P;2182-2302/Domain: C-type lectin homology <LCH>
P;2309-2365/Domain: complement factor H repeat homology <PHD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 170
                                                                                                                                                                                                                                    15.7%; Score 174; DB 1; Length 240
28.5%; Pred. No. 8e-07;
tive 23; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A47171; MUID:93300846; PMID:8314802
A;Accession: A47171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
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F;3296-3327/Domain: EGF homology <EGF>
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Best Local Similarity 28.5%
Watches 47; Conservative
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Best Local Similarity
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A; Micross-references: A2934
A; Map Poosition: Sq12-Sq4
C; Genetics: A3340
A; Map Poosition: Sq12-Sq4
C; Micross-references: A2934
A; Map Poosition: A1037
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A; Micross-references:
                                                                                                                     N'Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan N'Contains: glial hyaluronate-binding protein C.Species: Bome aaplens (man) ("Species: How aaplens (man) ("Species: How aaplens (man) ("Species: How aaplens (man) ("Species: How aaplens (man) ("Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 19-Jan-2001 ("Spacession: S06014; S43921; Ā60979; A30358; A29348; A45ī31; I54179 ("Simmermann, D.R.; Ruoslahti, E. BMO, "Species: Nulliple domains of the large fibroblast proteoglycan, versican. A; Reference number: S06014; MUID:90059882; PMID:2583089
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NCBIP:134457) core protein; C-type lecti

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A;Residues: 1-2327 <HER>
A;Residues: 1-2327 <HER>
A;Cross-references: EMBL:U76615; NID:g1730559; PID:g1730260; PIDN:AAB38524.1
A;Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; )
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; )
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycopr
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A.Residues: 1230-1249 <PB2>
A.Residues: 1230-1249 <PB2>
A.Residues: 1230-1249 <PB2>
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F.8-28/Domain: link protein repeat homology (fragment) <LNK2>
F.80-146/Domain: link protein repeat homology (fragments) <LNK3>
F.80-146/Domain: link protein repeat homology <LNK4>
F.167-248/Domain: C-type lectin homology <LCH>
F.1130-1250/Domain: C-type lectin homology <LCH>
F.11257-1313/Domain: Complement factor H repeat homology <FHD>
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Cispecies: Bos primigenius taurus (cattle)
Cipate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
Cispcession: T42630
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Submitted to the EMBL Data Library, September 1996
Alberting, T.M.; Kollar, J.; Huynh, T.D.
Submitted to the EMBL Data Library, September 1996
Alberting on mumber: Z22182
Alberting on mumber: Z22182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2165 NN---NAODYOWIGL-----NDKTIEGDFRWSDGHSLOFENWRPNOPDNFFATGEDC 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQPRNWYVDEP----SCGSEV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CVVMYHQPSAPAGIGGPYMPQWNDDRCNMKNNPICKYS----DEKPAVPSREAEGEETE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 QPVCRGG---TQRPCYKVIYFHDTSRRLNPEBAKBACRRDGGQLVSIESEDEQKLIEKPI
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                 A; Reference number: A91327; MUID: 85027710; PMID: 6489519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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26.8%; Pred. No. 9.6e-06;
iive 29; Mismatches 59
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Best Local Similarity 26.81
Matches 48; Conservative
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Best Local 8
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; D27751; E27751; F27
S;Antonsson, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 254, 16170-16173, 1989
A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of A;Reference number: A34234; MUID:89380219; PMID:2528543
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A;Mosiques: 1-28;59-82;131-137,'QSET',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
B;Perin, J.P.; Bonnet, F.; Jolles, P.
FBBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
C;Accession: T42710

WhWL, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996

A;Title: Characterization of a novel member of the macrophage mannose receptor type C l A;Accession: T42710

A;Reference number: Z22235; MUID:96355501; PMID:8702911

A;Reference rumber: Z22235; MUID:96355501; PMID:8702911

A;Accession: T42710

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1479 < WUNS-

A;Molecule type: mRNA

A;Residues: 1-1479 < WUNS-

A;Cross-references: EMBL:U56734; NID:91336073; PID:91336074; PIDN:AAC52729.1

C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II nC;Keywords: membrane protein; receptor

F;186-227/Domain: fibronectin type II repeat homology <2FR>
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Biochem. J. 243, 255-259, 198
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from
A;Reference number: A27752; MUID:87270630; PMID:3111460
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J. Biol. Chem. 266, 8198-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation
A;Reference number: A39808; MUID:91217051; PMID:2022637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 121
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A;Residues: 29-58;74130;174-175,'A',177-204;208-225 <PER>
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
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Best Local Similarity 31.4%;
Matches 48; Conservative 2;
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A;Residues: 128-621 <ANT>
A;Cross-references: GB:J05028
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A;Molecule type: mRNA
A;Residues: 622-1340 <OLD>
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A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
C;Genetics:
A;Gene: GB:AGC1; CSPG1; CSPGCP; MSX16
A;Gene: GB:AGC1; CSPG1; CSPGCP; MSX16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; E
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; E
C;Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracel
F;10-2416;Product: aggrecan cartilage long splice form #status predicted <WJ
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted <WJ
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
F;20-2162,2201-2319, 'A',2392-2415/Product: aggrecan short splice form #status predicted
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7;2302-2388/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,434,602,657,737,1889/Binding site: carbohydrate (Asn) (covalent) #sta
F;126,239,333,387,434,602,657,737,1889/Binding site: carbohydrate (Asn) (covalent) #sta
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted
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A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-612 <BEC>
A.Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
A.Cross-references: GB:M80778; NID:g193014; D.
A.Mol. Chem. 267, 15176-15183, 1992.
A.Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-select
A.Reference number: A42755; MUID:92340571; PMID:1378846
A.Status: nucleic acid sequence not shown
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A, Cross-references: GB:M87862, NID:9193107
A, Sxperimental source: endothelial cells
A, Note: sequence extracted from NCBI backbone (NCBIP:109470)
A, Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PID:9
A, Note: it is uncertain whether the initiator is Met-1 or the AUG codon preceding that C, Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology; C; Keywords: glycoprotein; transmembrane protein
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A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and fun A;Reference number: S23174; MUID:92283265; PMID:1375914
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C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: S23174; B42755
R;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2253 NN---NAQDYQWIGL-----NDRTIEGDFRWSDGHPMQFENWRPNQPDNFFAAGEDC 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2302 VVMIWHEKG------EWNDVPCNYHLPFTCKKGTVACGEPPVVEHARTFGQKKD 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;170-247/Domain: link protein repeat homology <LNK1>
P;268-349/Domain: link protein repeat homology <LNK2>
P;495-372/Domain: link protein repeat homology <LNK3>
P;593-673/Domain: link protein repeat homology <LNK4>
P;593-673/Domain: link protein repeat homology <LNK4>
P;677-861/Domain: keratan sulfate attachment #status predicted <KSA>
P;64-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
P;1511-2162/Domain: EGP homology <EGF>
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A/Pucleus: protein.
A/Residues: V. 404-405, XX. <FOS>
R/Budhaia, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
Biochem. J. 313, 933-940, 1996
A/Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A/Recession: S62786; MUID: 96190740; PMID: 8611178
A/Accession: S62786; MUID: 96190748; PIDN: CAA55463.1; PID: 970249
A/Forst references: EMBL: X17406; MID: 930248; PIDN: CAA55463.1; PID: 970249
A/FORDE: the nucleotide Sequence was submitted to the EMBL Data Library, January 1990
R/Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
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A/FILLE: A new epidermal growth factor-like domain in the human core protein for the lar
A/Reference number: A34226
A/Accession: A34226
A/Accession: A34226
A/Accession: BASO26
A/Residues: 1936-1963, VV, 1965-2069, VA, 2071-2415 < BAL>
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A; Residues: 361-370, X', 372-373;393-389, X', 401-407, X', 409 <SAN>
A; Residues: 361-370, X', 372-373;393-389, X', 401-407, X', 409 <SAN>
A; Cross-references: Plonic Abazoros: Plonic Abazoros: Plonic A; Plonic A; Plonic A; Plonic B; Ploni
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A,Accession: $46659
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 764-765, 4, 767-846, 7V, 848-862, X',864 <BAR>
A,Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A,Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A,Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
B,Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue
B,Ilic. M.Z., Mok, M.T., Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
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A,Title: Catabolism of aggreean by explant cultures of human articular cartilage in the A,Accession: $66389; MUID:96004775; PMID:7574678
C;Accession: A39086; S50206; A43919; S46659; S66389; S68646; S62786; A34226; B43919; C4:R;Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
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J. Saccession: A39086
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J. Saccession: S50206
J. Saccession: A39086
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Molecule this translation is not annotated in GenBank entry HSAGGREC, release 113.0
B;Sandy, J. J. Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
J. Clin. Invest. 89, 1512-1516, 1992
A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
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A; Residues: 17-23;24, XY, 26-27;393-401;402-403 <ILI>
R; Fossang, A.J.; Last, K.; Knaeuper, V.; Muxphy, G.; Neame, P.J.
FBBS Lett. 380, 17-20, 1996
A; Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A; Reference number: S68646; MUID:96181659; PMID:8603731
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A, Molecule type: pro
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A, Status: prelimina:
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Search completed: December 22, 2003, 16:14:41 Job time : \downarrow 0.9179 Bec8
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J. Biol. Chem. 262, 17768-1778, 1987
J. Biol. Chem. 262, 17768-1778, 1987
J. Stitle: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term A;Reference number: A28453; MUID:88087071; PMID:3693371
A;Accession: A28453
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Residues: 20-37,'W',39-60,'E',62-64,'X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A'
Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; E
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R; Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat A;Reference number: A23835; MUID:86250698; PMID:2424893
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                                                                                                                                                            Fi143-174/Domain: EGF homology < EGF>
Fi180-238/Domain: Complement factor H repeat homology < FH1>
Fi243-300/Domain: complement factor H repeat homology < FH2>
Fi305-363/Domain: complement factor H repeat homology < FH3>
Fi368-426/Domain: complement factor H repeat homology < FH4>
Fi368-426/Domain: complement factor H repeat homology < FH4>
Fi491-489/Domain: complement factor H repeat homology < FH5>
Fi491-548/Domain: complement factor H repeat homology < FH5>
Fi368-45-548/Domain: complement factor H repeat homology < FH5>
Fi359-35/391,528/Binding site: carbohydrate (Asn) (covalent) #status predicted
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1-19/Domain: signal sequence #status predicted <81G>
120-2124/Product: proteoglycan core protein #status predicted <MAT>
44-135/Domain: immunoglobulin homology <1PMM>
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A;Residues: 1-2124 <DOB>
F;Doege, K.; Sasak, M.; Horigan, E.; Hassell, J.R.; Yamada,
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
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:1-21/Domain: signal sequence #status predicted <SIG>:12-138/Domain: C-type lectin homology <LCH>:22-612/Product: P-selectin #status predicted <MAT>
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Species: Rattus norvegicus (Norway rat)
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A; Residues: 1856-2124 <DO2>
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F;126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status pre
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                                                                                                                                                                                                          7 QPVCRGG----TQRPCYKVIYPHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                         Length 2124;
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                                                                         DB 2;
                                                                  Query Match 13.9%; Score 153.5; DB 2
Best Local Similarity 26.3%; Pred. No. 4.5e-05;
Matches 47; Conservative 27; Mismatches 62
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US-09-087-0855-5

SGQUENCE 5, Application US/09087855

Patent No. US20020050310A1

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Immunex Corporation

TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES

FILE REFERENCE: 2003-083-08

CURRENT APPLICATION NUMBER: US/09/087, 855

CURRENT FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 6.7e-104;
iive 0; Mismatches 0;
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US-09-904-859-137
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ORGANISM: Homo sapiens
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Best Local Simi
Matches 204;
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US-09-887-855-5
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                                                                                                                                    December 22, 2003, 16:07:10 ; Search time 19.4937 Seconds (without alignments) 1954.412 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 GRLLSGQPVCRGGTQRPCYK......EBDAKKTFKESREAALNLAY 204
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| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/PCUS_PUBCOMB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:+
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| Cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:+
| Cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:+
                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-094-749-2090
US-10-094-749-2142
US-09-903-320-137
US-09-905-291A-137
US-09-905-291A-137
US-09-907-881-137
US-09-907-881-137
US-09-907-81-137
US-09-907-81-137
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US-09-907-81-137
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                         24 GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNPEBAKEACRRDGGQLVSIESEDEQKLIE 83
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APPLICANT: PATTERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: SHAH, Purvi
APPLICANT: SHAH, Purvi
APPLICANT: AL-, Preeti
APPLICANT: AU-YOUNG, Janice
APPLICANT: BURFORD, Neil
TITLE OF INVERNION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
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; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1
US-10-149-819-15
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100.0%; Score 1106; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 204; Conservative 0; Mismatches 0;
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                                                                                                                                                                                   100.0%; Score 1106; DB 12, 100.0%; Pred. No. 1.5e-103. ive 0; Mismatches 0;
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PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PROGram
SEQ ID NO 15
LENGTH: 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. Tom
                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2090
LENGTH: 374
                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 204; Conservative
NUMBER OF SEQ ID NOS: 3381
                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2090
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                                                                                                                        GENERAL INCORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Anderson, Dirk
APPLICANT: Anderson, Dirk
TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
FILE REPERENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1106; DB 9;
100.0%; Pred. No. 1.5e-103;
tive 0; Mismatches 0;
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APPLICANT: YOSHIYAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 6/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
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Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                   Sequence 2, Application US/09887855
Patent No. US20020058310A1
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
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Best Local Similarity 100.0
Matches 204; Conservative
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NAGAI, KEIICHI
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                  US-09-887-855-2
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-12-02

PRIOR PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

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PRIOR FILING DATE: 1999-12-02
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Paoni, Nicholas F.
                                                                                  Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
US20020132240A1
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; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-137
                                                                                                                                                                                                                                                                                                                                            Goddard, A.
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APPLICANT:
                                                     VMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLP 180
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APPLICANT: MAGAHARI, KENJI
APPLICANT: MASUHO, XASUHIKO
TITLE OF INVENTION: NOVEE FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: G0/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                          EETQEEDAKKTFKESREAALNLAY 204
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                                                                                                                                                                                                                                                                                                    Sequence 2142, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Best Local Similarity 99.5'
Matches 203; Conservative
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; ORGANISM: Homo sapiens
US-10-094-749-2142
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APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 6 US-09-909-320-137 ; Sequence 137, Application US/09909320

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84 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 204
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PLICATION NUMBER: PCT/US99/28313
PRIOR PLICATION NUMBER: PCT/US99/28313
PRIOR PLICATION NUMBER: PCT/US99/28564
PRIOR PLICATION NUMBER: PCT/US99/28565
PRIOR PLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLICATION NUMBER: PCT/US99/30095
PRIOR PLICATION NUMBER: PCT/US99/3091
PRIOR PLICATION NUMBER: PCT/US99/3099
PRIOR PLICATION NUMBER: PCT/US99/3099
PRIOR PLICATION NUMBER: PCT/US99/3099
PRIOR PLICATION NUMBER: PCT/US99/3099
PRIOR PLICATION NUMBER: PCT/US00/00219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher
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Filvaroff, Blen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanapeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
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APPLICANT: Abkenazi, Avi
APPLICANT: Betatelin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                   113 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 172
                                                                                                                                                       24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83
                                                                                                                       1 GRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                       Gaps
                                                                       9
           Length 382;
     98.7%; Score 1092; DB 10; Length ilarity 96.2%; Pred. No. 4e-102; Conservative 0; Mismatches 0; Indels
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PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
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PRIOR APPLICATION NUMBER: PCT/US99/21647
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CURRENT APPLICATION NUMBER: US/09/909,086B
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: 2000-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 137, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, A. Godowaki, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Kljavin, Ivar J. Kljavin, Ivar J. Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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        Query Match
Best Local Similarity
Matches 204; Conserv
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/665,350
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR PLING DATE: 1990-07-07
PRIOR PELING DATE: 1990-07-07
PRIOR PLING DATE: 1990-07-26
PRIOR PLING DATE: 1990-07-26
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                              Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary E
                                                                                                                                  Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: Homo Sapien

US-09-902-853-137
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: 10466-14

CURRENT APPLICATION NUMBER: 1040-07-12-99-05,291A

PRIOR PELING DATE: 1040-00-2-22

PRIOR PELING DATE: 1059-07-08

PRIOR PELING DATE: 1059-07-08

PRIOR PELING DATE: 1059-07-08

PRIOR PELING DATE: 1059-07-08

PRIOR PELING DATE: 1059-09-15

PRIOR PELING DATE: 1059-11-20

PRIOR PELING DATE: 1050-01-05

PRIOR PELING DATE: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRLLS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
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0; Mismatches 0;
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Publication No. US20020192659A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.2%;
Matches 204; Conservative C
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; ORGANISM: Homo sapiens
US-09-905-291A-137
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53 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
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96.2%; Pred. No. 4e-102;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 ELTTPVLPEETOEEDAKKTFKESREAALNLAY 235
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/2856
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-16
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PRIOR PLING DATE: 1999-13-30
PRIOR PLING DATE: 1999-13-30
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Grimaldi, Christopher J.
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Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 96.2°
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-907-824-137
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/065,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-09-13
                                                                                                                                                                                          53 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 112
                                                                                                                                                                                                                     84 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 143
                                                                                                                                                                                                                                                                                                                           144 SCGSEVCVVWYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 203
                                                                                                                                                                                                                                                                                              113 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 172
                                                                                                                    24 GRLLSASDLDLRGGGPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGLVSIES 83
                                                                                   1 GRLLS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
                                        Gaps
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          96.2%; Pred. No. 4e-102;
iive 0; Mismatches 0; Indels
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OR FILING DATE: 1999-09-08
OR PILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/20944
OR PILING DATE: 1999-09-15
OR PILING DATE: 1999-09-15
OR PILING DATE: 1999-09-15
OR PILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20020197671A1
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Stewart, Timothy A.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
          Best Local Similarity 96.2
Matches 204; Conservative
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Gao, Wei-Qiang
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APPLICANT:
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83

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53 EDEOKLIEKFIENLLPSDGDFWIGLRRREEKOSNSTACODLYAWTDGSISOFRNWYVDEP 112
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                                                                                                                                                                                                                                                                        APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILLING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR PLILNG DATE: 1000-02-22
PRIOR PLILNG DATE: 1999-07-07
PRIOR PLILNG DATE: 1999-07-28
PRIOR PLILNG DATE: 1999-07-28
PRIOR PLILNG DATE: 1999-07-28
PRIOR PLILNG DATE: 1999-09-09
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PRIOR PLILNG DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLILNG DATE: 1999-10-06
PRIOR PLILNG DATE: 2000-01-05
PRIOR PLILNG DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timcthy A.
Tumas, Daniel
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US-09-904-011-137
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Best Local Similarity
Matches 204; Conserva
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         APPLICANT: WOOD, Williams, F. MICKEY
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: DET/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLILNG DATE: 1999-09-15
PRIOR PLILNG DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLILNG DATE: 1999-09-15
PRIOR PLILNG DATE: 1999-10-05
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NUMBER OF SEQ ID NOS: 423
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o. US20030003530A1
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 96.23
Matches 204; Conservative
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COGANISM: Homo sapiens
US-09-907-841-137
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Publication No. US20
GENERAL INFORMATION:
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113 SCGSEVCVVMYHQPSAPAGIGGPYMPQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEBT 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83
                                                                                                                                                                                                                                                                                                                                                                                                                                           GRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES
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                                                                                                                                                                                                                                                                                                                                             Score 1092; DB 11; Length 382;
Pred. No. 4e-102;
0; Mismatches 0; Indels 8
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
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Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 96.2%;
Matches 204; Conservative
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Hillan, Kenneth, J
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Mather, Jennie P.
Pan, James
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Botstein, David
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Eaton, Dan L.
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                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                  US-09-906-742-137
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APPLICANT:
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                                                                                                                                                                                                                                    LENGTH:
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APPLICANT:

APPLICANT:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,742

CURRENT PILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PCT/US00/0414

PRIOR PILING DATE: 2000-09-18

PRIOR PLING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-30

                         SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 172
                                                  204 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                173 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 204
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                        Sequence 137, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard, A.
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                                                                                                                                                                                                                               RESULT 13
US-09-906-742-137
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APPLICANT:
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APPLICANT:
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24 GKLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-1
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
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PRIOR PELLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-09-08
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PRIOR PELING DATE: 2000-01-05
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Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth,
                            Filvaroff, Ellen
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Best Local Similarity 96.2
Matches 204; Conservative
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Tumas, Daniel
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ORGANISM: Homo sapiens
US-09-907-613-137
                                                                                                                                                                                                                                                                                                                                                                                                  James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 EDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
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24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIXFHDTSRRLNFEEAKEACRRDGGQLVSIES 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4e-102,
Ored. No. 1e-102,
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-26
PRIOR PLING DATE: 1999-09-08
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Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Best Local Similarity 96.2
Matches 204; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-906-838-137
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US-09-907-613-137
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APPLICANT:
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        Oy
        53 EDEQKLIEKFIENLLPSDGDFWIGLERREEKQSNSTACQDLYAWTDGSISOPRNWYVDEP 112

        Db
        84 EDEQKLIEKFIENLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISOFRNWYVDEP 143

        Oy
        113 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAGGET 172

        Db
        144 SCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAGGET 203

        Oy
        173 ELTTPVLPEETQEDAKKTFKESREAALNLAY 204

        Db
        204 ELTTPVLPEETQEEDAKKTFKESREAALNLAY 235

        Search completed: December 22, 2003, 16:16:47

        Job time: 19:4937 secs
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIINE=21085660; PubMed=11217851,

MEDIINE=21085660; PubMed=11217851,

A arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A hazawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A hazawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

B Aizawa T., Saturi Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo M., Aono H., Baddarelli R., Barsh G.,

Bakai K., Okido T., Puruno M., Aono H., Baddarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruchons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymbhaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Havashizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           bos taurus
mus musculu
                      nomo sapien
                                                      trimeresuru
                                                                          mus musculu
                                                                                           macaca mula
                                                                                                            papio hamad
                                                                                                                                                                anser anser
                                                                                                                                                                                                  bos taurus
                                                                                                                                                                               pongo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata, Vertebrata, Buteleostomi;
Sciurognathi, Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Function of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                  P07714
P05047
P23806
P43025
Q95198
Q28132
P43137
P83330
P98137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weng L., Smits P., Hubner R., Wouters J., Merregaert J., "Mt75, a low expressed c-type lectin gene involving in chondrogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chondrolectin precursor (Transmembrane protein MT75)
                                                                                                                                                                                                                                                                                                                                                          Q9CXM0; Q8VI31;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             273 AA
                                                                                                                                                                                                                                                       ALIGNMENTS
LEMI BOVIN
PSPA HUMAN
LECA SARPE
LIXA TRIFL
TETN MOUSE
LEMI MACMU
LEMI PAPHA
LITH BOVIN
LITH MOUSE
                                                                                                                                                           ANSAN
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata;
Mammalla; Butheria; Rodentia;
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NCBI_TaxID=10090;
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(c) 1993 - 2003 Compugen Ltd.
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CHOD_HUMAN
MANN_HUMAN
PGCN_MOUSE
PGCN_HUMAN
PGCV_BOVIN
PGCN_RAT
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seq length: 200000000
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EMBL; BC009418; AAH09418.1; -.
EMBL; AK022689; BAB14181.1; ALT_INIT.
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                                                       Nature 405:311-319(2000).
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Genew; HGNC:17807; CHODL.
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                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                          83 MLQNLTKPGTGISDGDFWIGLLRSGDQQT-SGACPDLYQWSDGSSSQFRNWYTDEPSCGS
                                                                                                                                                                                                                                                                               64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Hattori M., Fujiyama A., Taylor T.D.,
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Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weng L., Smits P., Wauters J., Merregaert J.;
Molecular cloning and characterization of human chondrolectin, a
novel type I transmembrane protein homologous to C-type lectins.";
Genomics 80:62-70(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09H9P2; Q9Hcv3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Chondrolectin precursor (Transmembrane protein MT75) (PRED12
                                                                                                                                                                                                                       DB 1; Length 273;
                                                                                                                                                                                                                                4.3e-44;
ches 41; Indels
                                                                                                         CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
N-LINKED (GLCNAC. ..) (POTYV -> M (IN REF. 2).
T -> K (IN REF. 2).
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E052D933F244F4C7 CRC64;
                                                      SMART: SM00034; CLECT: 1.
PROSITE: PS00615; CTYPE LECTIN 1; FALSE_NEG.
BCOSTE: PS550041; C_TYPE_LECTIN 2; 1.
Lectin; Transmembrane; Glycoprofein; Signal.
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                                                                                                                                                                                                                      51.5%; Score 574;
57.4%; Pred. No. 4.
         HSSP, P22897, 1EGG.
MGD, MGI:2179069, Chodl.
InterPro, IPR001304, Lectin_C.
                                                                                                                                                                                                   30303 MW;
EMBL; AK014255; BAB29226.1;
                                         Pfam; PF00059; lectin c; 1. SMART; SMO0034; CLECT; 1.
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Matches 109; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALSOUREDINE=22388257; PubMed=12477932;

Atausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atausher R.D., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B. Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
          Bloecker H.,
Dagand E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21564202; PubMed=11707072;
Reymond A., Friedli M., Neergard Henrichsen C., Chapot F., Deutsch S.,
Ucla C., Rossier C., Lyle R., Guipponi M., Antonarakis S.E.;
"From PREDs and open reading frames to cDNA isolation: revisiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ (S
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-i- TISSUB SPECIFICITY: Found in spleen, testis, prostate and fetal liver. Expression limited to vascular muscle of testis, smooth muscle of prostate stroma, heart muscle, skeletal muscle, crypts of small intestine, and red pulp of spleen.
-i- PTM: N-glycosylated.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isofaikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatahama M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Yakanabbi M., Chiba Y., Murakami K., Ishii S., Kawai Y., Saito K.,
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Ninomiya K., Iwayanagi T.;
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"The DNA sequence of human chromosome 21.";
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Genomics 78:46-54(2001).
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64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
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                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=92112893; PubMed=1730714;
Taylor M.E., Bezouska K., Drickamer K.;
"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=90324192; PubMed=2373685;
Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.;
"Primary structure of the mannose receptor contains multiple motifs resembling carbohydrate-recognition domains.";
J. Biol. Chem. 265:12156-12162(1990).
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Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
F4890AAFB572A311 CRC64;
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MEDLINE=93052405; PubMed=1294118;
Kim S.J., Ruiz N., Bazouska K., Drickamer K.;
"Organization of the gene encoding the human macrophage mannose receptor (MRC1).";
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"Structure of a C-type carbohydrate recognition domain from the
macrophage mannose receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVCVVMYHOPSAPAGIGGPYMFOWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                                                                          50.4%; Score 561.5; DB 1; Length 273; 60.1%; Pred. No. 5.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen).
                                                                                                                                                                                                                                                                                                                                25; Mismatches 35; Indels
                                                                                                                          CHONDROLECTIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Lectin; Transmembrane; Glycoprotein; Signal.
SIGNAL
CHAIN 22 273 CHONROLECTIN.
DOWAIN 217 237 POTENTIAL.
DOMAIN 238 273 CYTOPLASMIC (POTENTIAL)
DOMAIN 238 273 CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                             C-TYPE LECTIN.
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                                                                                                                                                                                                                                                   273 AA; 30431 MW;
                                                                                                                                                                                                                                                                                                                                  Matches 101; Conservative
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Genomics 14:721-727(1992).
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237
273
179
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P22897;
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CARBOHYD
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                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
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      RACANTITION
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
1. Biol. Chem. 275:21539-21548(2000).
2. I- FUNCTION: MEDIATER THE ENDOCYTOSIS OF GLYCOPROTEINS BY MACROPHAGES, IN SEVERAL RECOGNITION AND UPTAKE PROCESSES.
2. SUBCELLUAR LOCATION: Type I membrane protein.
3. CAREOHYDRATE. CRD 1-3 HAVE AT MOST VERY WEAK AFFINITY FOR CARBOHYDRATE. CRD 4 SHOWS THE HIGHEST AFFINITY BINDING AND HAS CHILSPECIFICITY FOR A VARIETY OF MONOSACCHARIDES. A LEAST 3 CRDS (4 5, AND 7) ARE REQUIRED FOR HIGH AFFINITY BINDING AND ENDOCATOSIS OF MULLITVALENT GLYCOCOMUGATES.
3. CHORD AND ARE REQUIRED FOR HIGH AFFINITY BINDING AND ENTRY: Contains 8 C-type lectin domains.
3. SIMILARITY: Contains 1 ricin B-type lectin domain.
3. SIMILARITY: Contains 1 ricin B-type lectin domain.
3. DATABASE: NAME=PROW: NOTE=PROW 2:85-89(2001);
3. WWW="http://www.ncbi.nlm.nih.gov/prow/guide/i64141515_g.htm".
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GO: GO: 0005887; C: Integral to plasma membrane; TAS.

GO: GO: 0005337; F: Receptor activity; TAS.

GO: GO: 0004872; F: Receptor activity; TAS.

GO: GO: 0004872; F: Receptor activity; TAS.

GO: GO: 0004873; Antiffeezell.

InterPro: IPR001363; Antiffeezell.

InterPro: IPR001304; Lectin C.

InterPro: IPR001304; Lectin E.

Pfam; PF00049; Inclin C.

Pfam; PF00049; Inclin C.

Pfam; PR00052; Ricin E. Bectin.

Pfam; PR00052; Ricin E. Bectin.

Pfam; PR00052; Ricin G. 8

PFINTS; PR0013; FNTYPEII.

PRINTS; PR0013; FNTYPEII.

PRODM; PR00095; FN TYPE II: 1.
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PDB; IEGG; 30-AUG-00.
PDB; IEGI; 30-AUG-00.
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M93212;
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M93219;
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139 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----- 187
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Brain;
MEDLINE=96039250; PubMed=7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
                                                                                                                                                                         PRT; 1268 AA
                                                                              MGD; MGI:10464; Cspg3.
InterPro; IPR00153; Antifreezell.
InterPro; IPR00153; Antifreezell.
InterPro; IPR001042; Bax hydroxyl.
InterPro; IPR001042; BGF 2.
InterPro; IPR00181; EGF 2.
InterPro; IPR00181; EGF 7.
InterPro; IPR00110; Ig-like.
InterPro; IPR00105; Ig-like.
InterPro; IPR001309; Ig-like.
InterPro; IPR001309; Ig-like.
InterPro; IPR001304; Lectin_C.
I.
Ffam; PP00004; Ig-like.
IPEm; PP00013; Xlink; 2.
                                                              188 -----BDAKKTFKESREAAL
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PRINTS; PR00356; ANTIFREEZEII.
ProDom; PD000918; Link; 2.
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PIR; S52781; S52781.
HSSP; P00740; 1EDM.
                                                                                                                                                                       STANDARD;
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Faessler R.;
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SMART; SM00459; RCIN; 1.

PROSITE; PS00615; C_TYPE_LECTIN 1; 6.

PROSITE; PS50041; C_TYPE_LECTIN 2; 8.

PROSITE; PS50023; FIBRONECTIN 2; 1.

PROSITE; PS50231; RICIN B_LECTIN, 2; 1.

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

RG1ycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.

SIGNAL

19 1456 MACROPHAGE MANNOSE RECEPTOR.
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                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
RICIN B-TYPE LECTIN.
C-TYPE LECTIN 1 (LONG FORM).
C-TYPE LECTIN 2 (LONG FORM).
C-TYPE LECTIN 3 (LONG FORM).
C-TYPE LECTIN 4 (LONG FORM).
C-TYPE LECTIN 5 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 7 (LONG FORM).
C-TYPE LECTIN 7 (LONG FORM).
C-TYPE LECTIN 8 (LONG FORM).
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909 ----MNDINCGYPNAFICQRHNSSINATTVMP-----TMPSVPSGCKEGWNFYSN 954
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-1- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
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-: SIMILARITY: Contains 2 EGF-like domains.
-: SIMILARITY: Contains 2 link domains.
-: SIMILARITY: Contains 1 C-type lectin family domain.
-: SIMILARITY: Contains 1 Sushi (SCR) domain.
-: SIMILARITY: DELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
CSPG3 OR NCAN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=99013874; PubMed=9795216;
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EMBL, AC003110; AAB86555.1; --
EMBL, AC005254; AAC25581.1; --
HSSP, PO0740; JEDM.
Genew; HGNC:2465; CSPG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Brain.
                                                        SEQUENCE FROM N.A.
           NCBI_TaxID=9606;
                77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 133
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R SMART; SM00032; CCP; 1.
R SMART; SM00034; CLECT; 1.
R SMART; SM00034; CLECT; 1.
R SMART; SM00109; IG; CCA; 1.
R SMART; SM00109; IG; CCA; 1.
R SMART; SM00145; LINK; 2.
R RPOSITE; PS00010; ASX HYDROXYL; 1.
R PROSITE; PS00010; ASX HYDROXYL; 1.
R PROSITE; PS00015; CTYPE_LECTIN_1; 1.
R PROSITE; PS00186; EGF_1; 3.
R RPOSITE; PS01187; EGF_CA; 1.
R PROSITE; PS01187; EGF_CA; 1.
R PROSITE; PS01241; LINK; 2.
R R PROSITE; PS01241; LINK; 2.
R R R STELLKE domain; Calcium; Repeat; Lectin; Suehi; Signal.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
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BY SIMILARITY.
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014594; Q9UPK6;
28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
CSPG3 OR NCAN OR NBUR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           DORNAL DON STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                       Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix. C., Andreise T., Trankheim M., Amico-Reller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Robayasahi A., Oleen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -: SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-: SIMILARITY: Contains 2 EGF-like domains.
-: SIMILARITY: Contains 2 link domains.
-: SIMILARITY: Contains 1 C-type lectin family domain.
-: SIMILARITY: Contains 1 Sushi (SCR) domain.
-: SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G., "Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
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InterPro; IRR000742; EGF 2.
InterPro; IRR001881; EGF 2.
InterPro; IRR0018181; EGF 2.
InterPro; IRR005109; EGF 11ke.
InterPro; IRR003109; EGF 11ke.
InterPro; IRR003599; IG 3.
InterPro; IRR001304; Lectin C.
InterPro; IRR0005389; Ink.
InterPro; IRR00005389; Ink.
InterPro; IRR00005389; Ink.
InterPro; IRR00005389; Ink.
InterPro; IRR00005389; Link.
Pfam; Pr000091; EGF; 2.
Pfam; Pr000091; EGF; 2.
Pfam; Pr00091; EGF; 2.
Pfam; Pr00091; IRR, 2.
Pfam; Pr00091; IRR, 2.
SMART; SM00034; CIECT; 1.
SMART; SM00034; CIECT; 1.
SMART; SM00044; ILINK; 2.
SMART; SM00445; LINK; 2.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; CTYPE LECTIN 1; 1.
PROSITE; PS00012; CTYPE LECTIN 1; 1.
PROSITE; PS00012; EGF 1; 3.
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Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
                         Zimmermann D.R.;
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
PROSITE; PS01187; Eur ..., _
PROSITE; PS0835; IG_LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
SIGNAL 1 22 POTENTIAL.
23 1321 NERROCAN CORE PROTEIN.
1921 IG-LIKE V-TYPE.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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P81282; 077609; 077610; 077611; 077612;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 IGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyaluronate-binding protein) (GHAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIŠSUE=Forebrain;
MEDLINE=98288320; PubMed=9624174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 31.5%;
Matches 45; Conservative 1
                                                                                                                                              356
1044
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1075:248-258(1991).
-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P81282-4; Sequence=VSP 003078, VSP 003081; IsSUE SPECIFICITY: Cerebral white matter. Vo and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; the major isoform v2 is restricted to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 link domains.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 1 EGF-like domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTECGLYCAN FAMILY.
                                                                                                                                                    SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                        TISSUE-Spinal cord;
MEDLINE-92062692; PubMed=1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic acid.";
    mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          central nervous system.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
the
"Versican V2 is a major extracellular matrix component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted, extracellular matrix. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with FBLN1 (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P81282-3; Sequence=VSP_003080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P81282-1; Sequence=Displayed;
                                                                            Biol. Chem. 273:15758-15764(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, 1FR001538; Link.
InterPro, 1PR000538; Link.
InterPro, 1PR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000152; Asx_hydroxyl
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR0005109; EGF_like.
InterPro; IPR001109; Ig-like.
InterPro; IPR001369; Ig.
InterPro; IPR0013096; Ig_MHC.
InterPro; IPR0013049; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF060456; AAC24358.1; -. BMBL; AF060457; AAC24359.1; -. EMBL; AF060458; AAC24360.1; -. EMBL; AF060459; AAC24361.1; -.
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Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin c; 1.
Pfam; PF00084; sushi; 1.
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PIR; T42389; T42389.
HSSP; P01132; 1EPG.
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Gaps

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3210 WIGL------NDKOMPEHDFRWTDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG-- 3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYYDEP----SCGSEVCVVMYHQPSAP
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TISSUB SPECIFICITY: BARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSED
IN KIDNEY, LUNG, LIVER AND MUSCLE.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroltin sulfate proteoglycan 3)
(245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIM=Spraque-Dawley; TISSUEB-Brain;
MEDLINE=92406907; PubMed=1326557;
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3311 KDGFIORHLPTIRCLGNGRWAMPKITCLNPSAYORTYSKKYFKNSSSAKDN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ETELTT-----PVL----PEETQEEDAKKTFKESREAALN 203
                                                                                                                                                                                                                                                                                                               15.7%; Score 174.5; DB 1; Length 3381; 25.5%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 AGIGGPYMPQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-----
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                                                                                                                                                                                                                                                                     AA; 369984 MW; F09716FA7778D459 CRC64;
                                                  /FTIGLUSP.003079.
Missing (in isoform V2).
/FTIGLUSP.003080.
Missing (in isoform V3).
/FTIGLUSP.003081.
MISSING (IN REF. 2).
N -> D (IN REF. 2).
C -> R (IN REF. 2).
           /FTId=VSP 003078.
Missing (In isoform V1)
/FTId=VSP_003079.
                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 4.5e-07; 26; Mismatches 71
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.5:
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                                   VARSPLIC
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PFam; PF00193; Xlink; 2.

R PRINTS; PR01265; LINKMODULE.

R PRINTS; PR001265; LINKMODULE.

R PRODOM; PD000918; Link; 2.

R SMART; SM00034; CLECT; 1.

SMART; SM00179; EGC CA; 1.

SMART; SM00179; EGC CA; 1.

R SMART; SM00179; EGC CA; 1.

R SMART; SM00179; EGC CA; 1.

R PROSITE; PS00101; ASX HYDROXYL; 1.

R PROSITE; PS00101; ASX HYDROXYL; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS01187; EGF CA; 1.

R PROSITE; PS01187; EGF CA; 1.

R PROSITE; PS01187; EGF CA; 1.

R PROSITE; PS01241; LINK; 2.

R PROSITE; PS01241; LINK; 2.

R Alycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.

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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
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EGF-LIKE 2, CALCIUM-BINDING
C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSICAN CORE PROTEIN. IG-LIKE V-TYPE.
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                                                                                                                                                            O-LINKED (XYL. . .) (CHONDROITIN SULPATE)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Wistar Kyoto;
MEDLINE=9930804; PubMed=9642104;
Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding
proteoglycans in developing brain: aggrecan, versican, neurocan, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 349-2738 FROM N.A. (ISOFORM VO), SEQUENCE FROM N.A. (ISOFORM V3), AND SEQUENCE OF 2657-2738 FROM N.A. (ISOFORM VINT) STRAIN-MISTEAR KYOLO, MEDLINE=99327053; Pubmed=10397680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGCV_RAT STANDARD; PRT; 2738 AA.
O9RERE4; 008592; 088564; 09R1K4;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
(Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
hyaluronate-binding protein) (GHAP) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98094159; PubMed=9434070; Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.; Proteoglycan expression in the normal rat kidney."; Nephron 77:461-470(1997).
                                                                                                                  .) (POTENTIAL)
                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                         15.6%; Score 174; DB 1; Length 1257; 30.8%; Pred. No. 1.5e-07; ive 18; Mismatches 49; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wight T.N.;
"Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
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Biochem. Biophys. Res. Commun. 247:207-212(1998)
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM-BINDING (POTENTIAL)
 CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
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150 kDa ADULT CORE GLYCOPROTEIN.
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InterPro; IPR001309; Ig.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00008; EGF; 2.
Pfam; PP000047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002353; Antifreezell.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR001742; EGF~2.
InterPro; IPR001881; EGF~2.
InterPro; IPR005209; EGF~like.
InterPro; IPR007110; IG-like.
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PF00059; lectin_c; 1.
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Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
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ISOId=09ERB4-3; Sequence=VSP 003092;
-!- TISSUE SPECIFICITY: In kidney is expressed in the papillary area,
but not in glomeruli.
-!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
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                                                                                                                                                                               -1- SUBURIT: Interacts with FBLN1 (By similarity).
-1- SUBURIT: Interacts with FBLN1 (By similarity).
-1- ALTERNATIVE PRODUCTS:
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                   IsoId=Q9ERB4-2; Sequence=VSP_003091;
                                                                                                                                                                                                                                                                                 IsoId=Q9ERB4-1; Sequence=Displayed;
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SMART; SM00034; CLBCT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS00010; ASX_HVDROXYL; 1.
PROSITE; PS00010; ASX_HVDROXYL; 1.
PROSITE; PS00011; C_TYPE_LECTIN ; 1.
PROSITE; PS00041; C_TYPE_LECTIN 1; 1.
PROSITE; PS00041; C_TYPE_LECTIN 2; 1.
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InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi SCR_CCP.
PRINTS; PR01265; LINKWODULE.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR007110; Ig-like.
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EMBL, U75306; AAB51125.1; --
EMBL, AF08454; AAD48544.1; --
EMBL, AF072892; AAC26116.1; --
EMBL, AY007691; AAG16631.1; --
HSSP; P01132; IEPG.
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EGF 2, 1.

EGF CA, 1.

IG_LIKE, 1.
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PROSITE; PS01186;
PROSITE; PS01187;
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PROSITE; PS01241;
                                                                                                                                                                                                                                                                   Name=V0;
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2567 WIGL------NDKMFEHDFRWTDGSALQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2616
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R -> RKWSFRKNGQPCFNKY (in isoform Vint).
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15.6%; Score 174; DB 1; Length 2738;
Best Local Similarity 28.5%; Pred. No. 3.9e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 46
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                                                                                                                                                                                                                                                                                                    EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING.
C-TYPE LECTIN.
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2738 AA; 300004 MW; 12CA626D58BD8C6A CRC64;
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acid; Alternative splicing.
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IsoId = Q62059-2; Sequence = VSP_003087, VSP_003088;
                                                          Name=V3;
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 SEQUENCE OF 1-1692 FROM N.A. (ISOFORM VI).

SEQUENCE OF 1-1692 FROM N.A. (ISOFORM VI).

STRAIN=C57BL/6J; TISSUB=Skin;

MEDIINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Fukunishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. BEOL. Chem. 274:2044-20449 (1999).

-1- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-1- SUBDINIT: Interacts with FBLNI.
-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6;
MEDLINE=95181355; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alteratively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D., "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                          PGCV_MOUSE STANDARD; PRT; 3358 AA.
062059; Q62058; Q9CUUD;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS VO; VI AND V2).
STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
MEDLINE=9512251; PubMed=782336;
Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
"Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q62059-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                tissues.";
J. Biol. Chem. 270:3914-3918(1995)

    Biol. Chem. 270:958-965(1995).

                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM V3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH FBLN1.
                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                         NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10400671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
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RESULT 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 ISOId=062059-4; Sequence=VSP 003087, VSP 003090;
-1-TISSUE SPECIFICITY: V2 is found only in brain.
-1-DEVELOPMENTAL STAGE: Disappears after the cartilage development.
-1-SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1-SIMILARITY: Contains 2 link domains.
-1-SIMILARITY: Contains 1 C-type lectin family domain.
-1-SIMILARITY: Contains 1 Sushi (SCR) domain.
-1-SIMILARITY: Contains 1 Sushi (SCR) domain.
-1-SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL)
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SIGNAL 1 POTENTIAL.
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VERSICAN CORE PROTEIN.
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Isold=Q62059-3; Sequence=VSP_003089;
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PRODOM; PROUSES, LINKWODULE.
PRODOM; PRO00918; Link; 2.
SWART; SW00034; CCP; 1.
SWART; SW00034; CCP; 1.
SWART; SW0049; EGF_CA; 1.
SWART; SW00409; EGF_CA; 1.
SWART; SW00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00015; C_TYPE_LECTIN_1; 1.
PROSITE; PS01186; EGF_2; 1.
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EMBL; D28599; -; NOT ANNOTATED CDS.
EMBL; D22604; BAA06802.1; -.
EMBL; AK01425; BAB29411.1; -.
HSSP; P01132, 1EPG.
MGJ: 102899; Cepg2.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0010152; Asx hydroxyl.
InterPro; IPR0010152; Asx hydroxyl.
InterPro; IPR0010152; BGF_2.
InterPro; IPR001019; IGP_Ca.
InterPro; IPR001010; IGP_Ike.
INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTE
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TISSUE-Brain;
MEDLINE-95181355; PubMed-7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"xxpression of PG-M(V3), an alternatively spliced form of PG-M without a chondroltin sulfate attachment in region in mouse and human tissues.";
J. Biol. Chem. 270:3914-3918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krusius T., Gehlsen K.R., Ruoslahti E.,
"A fibroblast chondroitin sulfate proteoglycan core protein contains
lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=90659882; PubMed=2583089;
MEDLINE=90659882; PubMed=2583089;
MEDLINE=90659882; PubMed=2583089;
Multiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mapping of the versican proteoglycan gene (CSPG2) to the long arm human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                         SEQUENCE FROM N.A. (ISOFORM VO).
MEDLINE=95105188; PubMed=7528742;
MABO M.F., Zimmermann D.R., Iozzo R.V.;
"Characterization of the complete genomic structure of the human versican gene and functional analysis of its promoter.";
"J. Biol. Chem. 269:32999-33008(1994).
   (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM V2).

TISSUE-Glial tumor;

MEDLINE=95105187; PubMed=7806529;

Bours-Zimmermann M.T., Zimmermann D.R.;

A novel glycosaminoglycan attachment domain identified in two alternative splice variants of human versican.";

J. Blol. Chem. 269:32992-32998(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lemire J.M., Braun K.R., Maurel P., Kaplan B.D., Schwartz S.M.,
Wight T.N.;
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of a glial
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MEDLINE=93122792; PubMed=1478664;
IO2ZO R.U., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Versican/PG-M isoforms in vascular smooth muscle ce
Atterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999)
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MEDLINE=89174663; PubMed=2466833;
Perides G., Lane W.S., Andrews D., Dahl
"Isolation and partial characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Aortic smooth muscle;
MEDLINE=99327053; PubMed=10397680;
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J. Biol. Chem. 264:5981-5987(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2711-3396 FROM N.A.
TISSUE-Lung fibroblast;
MEDLINE=88007514; PubMed=2820964;
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MEDLINE=96213482; Pubmed=8627343;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM VI).
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                                                 Homo sapiens (Human)
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P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1997 (Rel. 35, Requence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
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/FIId=VSP 003090.

A -> G (IN REF. 3),

MISSING (IN REF. 3),

I -> T (IN REF. 3),

TVWNSNS -> OFGIQTA (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
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PGCV HUMAN
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Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.n.,
"Differential expression of versican isoforms in brain tumors.";
"Neuropathol. Exp. Neurol. 55:28-531(1996).
-! FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-! SUBGNIT: Interacts with FBLNI (By similarity).
-! SUBCELULAR LOCATION: Secreted; extracellular matrix.
-! ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=5;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                              MIM; 118661; -. GO CONTROLL OF TABLE MAIN; TABLE OF GO: GO: 0005578; C: extracellular matrix; TAB.

GO; GO: 0005540; F: chondroitin sulfate proteoglycan; TAB.

GO; GO: 000540; F: hyaluronic acid binding activity; TAB.

GO; GO: 000540; F: hyaluronic acid binding activity; TAB.

GO; GO: 0007275; P: peavelopment; TAB.

InterPro; IPR000125; ABx. hydroxyl.

InterPro; IPR000152; ABx. hydroxyl.

InterPro; IPR006209; EGF_Ca.

InterPro; IPR006209; EGF_like.
                                                                                                                                                          IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
                                                                                                                                                                                                    IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
                                                                                                                                                                                IsoId=P13611-3; Sequence=VSP_003084;
                                                                                                                                                                                                                        IsoId=P13611-5; Sequence=VSP_003086;
                                                                                                                                       IsoId=P13611-1; Sequence=Displayed;
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InterPro; IPR001304; Lectin_C.
InterPro; IPR000539; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U16306; AAA65018.1; --
EMBL, X15998; CAA34128.1; --
EMBL, S25488; AAB24878.1; --
EMBL, U36555; AAA67565.1; --
EMBL, D32039; BAA06801.1; --
EMBL, AC0814; AAA36437.1; --
EMBL, AF084545; AAA48645.1; --
PIR, S06014; A60979.
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Pfam; PF00059; lectin c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
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MIM; 118661; -.
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3177 QGQCYK--YF---AHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRV-----GHDYQ 3224
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
GAG-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein, Proteoglycan, Lectin, Extracellular matrix, Sushi, Signal, Repeat, EGF-like domain, Calcium, Immunoglobulin domain, Hyaluronic acid, Alternative splicing.

1 POTENTIAL.
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; Pred. No. 5.1e-07;
23; Mismatches 55;
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PGCV_CHICK
ID PGCV_CHICK STANDARD; PRT; 3562 AA.
AC Q90953; Q90945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
ProDom; PD000918; Link; 2.
SMART; SM00032; CCF; 1.
SMART; SM00013; CCET; 1.
SMART; SM00179; EGF CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX HYPROXYL; 1.
PROSITE; PS00041; C_TYPE_LECTIN 1; 1.
PROSITE; PS00041; C_TYPE_LECTIN 2; 1.
PROSITE; PS001186; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF 2; 1.
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LINK 2.
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28.5%;
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                                                                                                             STRAIN=White leghorn; TISSUB=Limb bud;
MEDLINE=933000846; PubMed=8314802;
Shinomura T., Nishida Y., Ito K., Kimata K.;
Shinomura T., Nishida Y., Ito K., Kimata K.;
Shinomura T., Nishida Y., Ito K., Kimata K.;
shinomura Conting of Pola, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative spliced multiforms of Fg-M and their relationships to versican.";
J. Biol. Chem. 268:14461-14469(1993).
-I- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                             developing limb buds.
 Versican core protein precursor (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                   Isold=Q90953-2; Sequence=VSP_003093;
TISSUB SPECIFICITY: Prechondrogenic condensation area of
                                                                                                                                                                                                                                         SÜBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                  IsoId=090953-1; Sequence=Displayed;
                                                                                                     SEQUENCE FROM N.A. (ISOFORMS VO AND VI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR000152; Asx hydroxyl.
InterPro; IRR000142; EGF 2.
InterPro; IRR001881; EGF 7a.
InterPro; IRR001801; EGF 1ike.
InterPro; IRR00110; IG-like.
InterPro; IRR001599; IG
InterPro; IRR001599; IG
InterPro; IRR001304; Lectin_C.
InterPro; IRR0001304; Link.
InterPro; IRR0001416; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00008; EGF; 2.
Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin c; 1.
Pfam; PF00084; suehi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR01265; LINKMODULE.
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SM00032; CCP; 1.
SM00034; CLECT; 1.
SM00179; EGF CA; 1.
SM00409; IG; 1.
                                  Gallus gallus (Chicken)
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HSSP; P00740; 1EDM.
                                                                              NCBI_TaxID=9031;
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SMART; SM00034;
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MEDINE=205070883; PubMed=10334210;

MEDINE=205070883; PubMed=10334210;

Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;

Molecular and cellular properties of the rat AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, a C-type of the rat. AAA antigen, and C-type of the rat. AAA antigen, and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction and construction a
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3390 WIGL------NDKMFERDFRWTDGSPLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
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MEDLLNE=20545-218; Pubmed=110931122;
Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
"Characterization and molecular cloning of rat C1qRp, a receptor on NK
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
Complement component Clq receptor precursor (Complement component Clq receptor precursor (Complement component Clq (CD93 annigen) (C1qR(p)) (C1qR(p)) (C1q/MBL/SPA receptor)
(C1093 annigen) (Cell surface antigen AA4).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Eur. J. Immunol. 30:3355-3362(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 WYKASKSSCISKRCVSLILDLSLKPHPSHLP-----KWHESPCGTPDAPGNSIEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGCA_BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; Q28159;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                                                                                                                       COMPLEMENT COMPONENT C1Q RECEPTOR. EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 1; Length 643; 4.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73; Indels
                                                                                                                                                         Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9AE4C933AD943DB6 CRC64;
                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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                                               PROSITE; SMO0179; EGF CA; 3.
PROSITE; PS001019, AZX HYDROXL; 3.
PROSITE; PS00615; C TYPE_LECTIN 1; PALSE_NEG.
PROSITE; PS50041; C TYPE_LECTIN 2; 1.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01186; EGF CA; 3.
PROSITE; PS01186; EGF CA; 3.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS01187; EGF CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IN REP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 4.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 LCKFNFKGMCSPLALGGPGQLTYTTP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68781 MW;
Pfam; PF00008; EGF; 5.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%;
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                                                                                                                                                                                                                                                                                                                 417 4
643 AA;
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SIMILARITY:

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DOMAIN: TWO GLOBULAR DOMAINS, GI AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE C-TERMINUS, GI CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULETDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS, G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 563-1056 FROM N.A.
MEDLINE=89380219; PubMed=2528543;
Antonason P., Heinegaard D., Oldberg A.;
"The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.";
"J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perin J.-P., Bonnet F., Jolles J., Jolles P.;
"Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligomolectide probe.";
FEBS Lett. 176:37-42(1984).
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                  MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan,
deduced from a cDNA clone, contains numerous Ser-Gly sequences
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cartilage;
MEDLINE=9335255; PubMed=8349621;
Fueloep C., Walcz B., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                     SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                       SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P13608-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 268:17377-17383(1993).
                                                                                                                                                                                                                                                                                                                                               arranged in homologous repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85027710; PubMed=6489519;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2114-2150 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 243:255-259(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bimilarity).
ALTERNATIVE PRODUCTS:
                 taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE.
                                                                         NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2
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PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED ASSOT 40) OLICOSACCHARIDES.
PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN ADULT AND FETAL BOVINE PROTEOGLYCANS.

AND G3

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                     -!- SIMILARITY: Contains 4 link domains.
-!- SIMILARITY: Contains 1 BGF-11ke domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA APPROXIMATE TANDEM REPEATS OF
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EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
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R SMART; SM0013; CCP; 1.

R SMART; SM0013; CCE; 1.

R SMART; SM0013; CCE; 1.

R SMART; SM0013; CEECT; 1.

R SMART; SM00145; LINK; 4.

R PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

R PROSITE; PS00015; C_TYPE_LECTIN_2; 1.

R PROSITE; PS00187; GG_I; 1.

R PROSITE; PS00296; IG_LIKE; 1.

R PROSITE; PS01296; IG_MC; FALSE_NEG.

R PROSITE; PS01296; IG_MC; FALSE_NEG.

R PROSITE; PS0121; LINK; 1.

R PROSITE; PS0121; LINK; 1.

R PROSITE; PS0124; LINK; 1.

R PROSITE
  Contains 1 immunoglobulin-like V-type domain
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AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
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LINK 4.
23 X 6 AA APPRO)
E-[EK]-P-F-P-S.
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SUSHI.
                                                                                                                                                                                                                                                                                                PIR; A44234; A39808.
PIR; A44234; A39808.
PIR; T42630; T42630.
HSSP; P08709; 18F9.
                                                                                                                                                                                                                                                                                                                                                                                                           Antifreezell.
Ask hydroxyl.
EGF-2.
EGF-Ca.
EGF-Tike.
Ig-Tike.
Ig-MC.
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Pfam; PF00059; lectin c; 1.
Pfam; PF001059; lectin c; 1.
Pfam; PF001084; sushi; 1.
Pfam; PF001094; Xlink; 4.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Link. SGXXSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IRR00142; EGE
InterPro; IRR001881; EGE
InterPro; IRR001801; EGE
InterPro; IRR003006; Ig-
InterPro; IRR003006; Ig-
InterPro; IRR001304; Leci
InterPro; IRR00538 Lini
InterPro; IRR003324; SGX
InterPro; IRR00538 Lini
InterPro; IRR00538 Lini
InterPro; IRR00538 Lini
InterPro; IRR00538 Lini
InterPro; IRR00538 Lini
InterPro; IRR00548 SGX
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22364
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InterPro; IPR000152;
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2114
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Interpro; IPR007110; Ig-like.
Interpro; IPR003599; Ig.
Interpro; IPR001006; Ig.MHC.
Interpro; IPR001304; Lectin_C.
Interpro; IPR000538; Link.
Interpro; IPR0004324; SGXXSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; lectin_c; 1.
; SGXXSG; 71.
; sushi; 1.
; Xlink; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:319; AGC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00084;
Pfam; PF00193;
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                                                                                                                                                                                                                                                                                                                                                                     Name=3;
                                                                                                                                                                                                                                                                                                   Name=1;
                                                                                                                                                                                                                                                                                                                                    Name=2
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      2202 NN---NAQDYQWIGL------NDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDC 2250
                                                                                                                                                                                                                                                                                                                                                                                                                   66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 QPVCRGG---TQRPCYKVIYFHDISRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGCA HUMAN STANDARD; PRT; 2415 AA.
P16112; Q13650;
01-APG-1990 (Rel. 14, Created)
01-APG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).

MEDLINE=89380154; PubMed=2789216;

MEDLINE=89380154; PubMed=2789216;

"A new epidermal growth factor-like domain in the human core protein for the large cartilage-specific proteoglycan. Evidence for allernative epilcing of the Gomain.";

J. Biol. Chem. 264:1574-15750(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Chondrocytes; Managa Y.; Branda Y.; Branda Y.; Branda Y.; Booge K.J., Saaski M., Kimura T., Yamada Y.; Complete coding sequence and deduced primary structure of the hums complete coding sequence and deduced primary structure of the hums cartilage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms."; J. Blol. Chem. 266:894-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                 DB 1; Length 2364;
                                                                                                                                                                                                                                                                                                                                                                 59; Indels
                                                                                                                                                                                                                                                                                                6FF83763420C3D4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Chondrocytes;
Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.
CLINED (GLCNAC...) (P.
N-LINED (GLCNAC...) (P.
N-LINED (GLCNAC...) (P.
N-LINED (GLCNAC...) (F.
N-LINED (GLCN
                                                                                                                                                                                                                                                                                                                               Score 158.5; DB 1
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1778-2415 FROM N.A. (ISOFORM 2).
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Σ
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                                                                                                                                                                                                                                                                                                  2364 AA; 246359
                                                                                                                                                                                                                                                                                                                                                                 48; Conservative
                                    554
682
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                                    533
607
607
2117
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2250
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CARBOHYD
                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P16112-3; Sequence=VSP 003074, VSP 003075; DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULPATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2.
                                                                                                                                                           CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
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SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 4 link domains.

SIMILARITY: Contains 1 EGF-like domain.

SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 1 Sushi (SCR) domain.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                          Barry F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO: 0005204; F: chondroitin sulfate proteoglycan; TAS.
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Comment=Additional isoforms seem to exist;
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InterPro, IPR006209; EGF like.
InterPro, IPR006210; IEGF.
                                TISSUE=Blood;
MEDLINE=95128522; PubMed=7827755;
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EMBL; J05062; AAA35726.1; -.
EMBL; X17406; CAA35463.1; -.
EMBL; S74659; AAC60643.2; -.
PIR; A39086; A39086.
SEQUENCE OF 764-864 FROM N.A.
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PRINTS; PRO1265; LINKMODULE.
R PRINTS; PR01365; ANTIFREEZEII.
R PRODOM; PD0100919; Link; 4.
R SWART; SM00032; CCP; 1.
SWART; SM00049; Link; 4.
SWART; SM00049; Link; 4.
R SWART; SM00049; Link; 4.
R SWART; SM00049; Link; 4.
R SWART; SM000409; Link; 4.
R PROSITE; PS000415; C_TYPE_LECTIN_1; 1.
R PROSITE; PS000415; C_TYPE_LECTIN_2; 1.
R PROSITE; PS00022; EGF 1: 1.
R PROSITE; PS00290; IG_MRC; 1.
R PROSITE; PS00290; IG_MRC; 1.
R PROSITE; PS00290; IG_MRC; 1.
R PROSITE; PS00290; IG_MRC; 1.
R PROSITE; PS00290; IG_MRC; 1.
R PROSITE; PS01291; Link; 3.
W Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushi; Ternative Epilicing; Repeat; Immunoglobulin domain.
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C-TYPE LECTIN.
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TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYDURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

TO SUBCELLULAR DOCATION: Secreted; extracellular matrix (By atmilarity).

TERMINOS OF THE RROTECCLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTENTS LINK DOMAINS AND THUS SCONSISTS OF THREE DISJURIDES—BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B, B, MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
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                                                                                                                                                9 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIESEDEQKLIEKFI
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028343; 02810;
01-007-1997 (Rel. 35, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
AGGTECAN CORE protein precursor (Cartilage-specific proteoglycan core protein) (CSPCF).
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Canis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                 Length 2415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Cartilage,
MEDLINE=95128522; PubMed=7827755;
Barry R.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Glant T.T., Adams M.B., Kwok S.X.F., Huang D., Fueloep C.;
"Complete coding sequence and deduced amino acid sequence of canine cartilage.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1830-2333 FROM N.A.
Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.,
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                           Indela
2391 2391 A -> P (IN RBF. 2 AND 3).
2415 AA; 250191 MW; 1288937E1B98C6B6 CRC64;
                                                               14.2%; Score 158.5; DB 1; 29.1%; Pred. No. 8.1e-06;
                                                                                                        22; Mismatches 62;
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Matrix Biol. 14:323-328(1994).
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                                                                                   Best Local Similarity 29.14
Matches 52; Conservative
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2171 NN---NAQDYQWIGL------NDRTIEGDFRWSDGHSLQFENWRPNQPDNFFVSGEDC 2219
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Job time : 6.56161 secs
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         -i- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N.LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-i- SIMILARITY: Contains 1 link domains.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
-i- SIMILARITY: Contains 1 Sushi (SCR) domain.
-i- SIMILARITY: Contains 1 Sushi (SCR) domain.
-i- SIMILARITY: Contains 1 SGF-like domain.
-i- SIMILARITY: CONTAINS 1 SGF-like domain.
THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
LINK 1.
LINK 2.
LINK 3.
LINK 4.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
G1-A.
G1-B.
G1-B.
G2-B.
KS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U65989; AAB06238.2; -... EMBL; L07054; -... EMBL; L07054; -... NOT_ANNOTATED_CDS. PIR; 146998; 146998. HSSP; P08709; 1BF9. InterPro; IPR000152; A8x hydroxyl. InterPro; IPR000152; A8x hydroxyl. InterPro; IPR001891; EGF_2. InterPro; IPR001891; EGF_1; InterPro; IPR001909; EGF_1ike. InterPro; IPR005100; EGF_1ike. InterPro; IPR005100; EGF_1ike. InterPro; IPR0031006; Ig_MHC.
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2249
AND THE
AND G3.
PTM: COI
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65

Tue Dec 23 09:37:13 2003

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein December 22, 2003, 16:06:34; Search time 10.0151 Seconds (without alignments) 1978.090 Million cell updates/sec Run on:

1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206 US-09-887-855-2_COPY_22_227 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	Description	resolution and the second and the se		- mouse	versican precursor			versican precursor		chondroitin sulfat	mannose receptor.	proteoglycan core	addrecan - bovine	addrecan precursor	E-selectin precurs	proteoglycan core	brevican precureor	hypothetical prote	IdE Fc receptor II	brevican - human (aggrecan precursor	protein F52E1.2 (i	brevican precursor	lectin BRA3-1 prec	addrecan precureor	SCAVENGER recentor	brevican predurent	lectin - barnacle		1117 - 117 - 117
NO S	ID	A36563	A48925	S52781	T14274	T42389	S28764	A55535	A60979	A47171	T42710	A39808	T42630	A39086	B42755	A28452	A54423	T24425	LINHUER	T46256	A55182	E89130	S57653	LNRC1	I50421	JC7595	549126	S10548	\$23936	ACCANA
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æ	Query Match	16.3	16.0	15.9	15.7	15.7	15.6	15.6	15.6	15.3	15.3	14.2	4	14.2	3	13.8	13.6	13.4	13.4	13.3		•	13.2	ω.	'n.	13.0	13.0	13.0	13.0	13
	Score		178.5	177	174.5	174.5	174	174	174	171	170.5	158.5	158.5	158.5	154.5	153.5	152	149.5	149	148.5	148.5	148	14	٠	4	145.5	145	₹.	144.5	111
	Result No.	-	7	e	4	S	ø	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	000

coagulation factor	L-selectin precurs	hypotherical prote	bitiscetin alpha c	phospholipase-A(2)	IgE Fc receptor, 1	lectin BRA3-2 prec	. L-selectin precurs	pulmonary surfacta	pulmonary surfacta	pulmonary surfacta	lectin precursor -	coagulation factor	tetranectin precur	hypothetical prote	IqE Fc receptor II
JC4329	A32375	T26655	JC5058	S48719	LINMSER	LNRC3	S22124	LINHUPS	LNHUP6	LNHUP1	LNFHLS	JC4690	JC4031	T29200	S34198
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	143.5 12			142	141.5	140.5	140	139	139	139	139	138.5	138.5	138	137.5

ALIGNMENTS

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mannose receptor precursor. Annuan
Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cipecession: A36563; A60926; A44255; B44255; Biol. Chem. 265, 12165-12162, 1990
A; Title: Primary Structure of the mannose receptor contains multiple motifs resembling A; Reference number: A36563; MUID:90324192; PMID:2373685
A; Mocession: A36563; MUID:90324192; PMID:2373685
A; Residues: 1-1456 <TAY>
A; Residues: 1-1456 <TAY>
A; Residues: 1-1456 <TAY>
A; Residues: 1-142; Thas-1985-1794; Bailly. P: Warner, A.
B; Ezekowitz, R.A.B.; Sastry, K.; Bailly. P: Warner, A.
B; Ezekowitz, Bailly. Bacquence including the amino end of the mature protein, were con R; Ezekowitz, R.A.B.; Sastry, K.; Bailly. P: Warner, A.
B; Reference number: A60926; MUID:91079783; PMID:2258707
A; Residues: 1-1333, Tr, 1335-1456 <EZES
A; Molecule type: mRNA
A; Residues: 1-1333, Tr, 1335-1456 <EZES
A; Note: translation of the nucleotide sequence is incomplete
A; Rim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A; Rim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A; Rith, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
A; Reference number: A44555; MUID:93052405; PMID:1294118
A; Reference number: A44555; MUID:93052405; PMID:1294118
A; Reference number: A44555; MUID:93052405; PMID:1294118
mannose receptor precursor - human
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A,Status: preliminary; nucleic acid sequence not shown; not compared with conceptual t: A,Molecule type: DNA K,Molecule type: DNA K,Residues: 155-233, KSAL',238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865 A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:11842) A;Gene: GDB:MRC1 A;Cross-references: GDB:133759; OMIM:153618

A Map position: 10p13-10p13
C; Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
C; Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
C; Keywords: duplication; lectin; tandem redicted <SIG>
C; Keywords: duplication; lectin; tandem redicted <SIG>
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 168-209/Domain: fibronectin type II repeat homology <2FI>
F; 223-340/Domain: C-type lectin homology <LCHI>
F; 362-486/Domain: C-type lectin homology <LCHI>
F; 945-1079/Domain: C-type lectin homology <LCHI>

Gaps 54; Query Match 16.3%; Score 182; DB 1; Length 1456; Best Local Similarity 25.5%; Pred. No. 9.1e-08; Matches 52; Conservative 37; Mismatches 61; Indels 54

8

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neurocan - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: JP-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: 552781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
A;Description: Amino acid sequence of mouse neurocan and brevican and their different e
A;Reference number: 552781
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C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14274
R;Schmalfeldt, M; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine bra
A;Reference number: 217954; MUID:98288320; PMID:9624174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mLNA
A;Cross-references: BMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g758630
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: BGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
F;1167-1223/Domain: complement factor H repeat homology <FHD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1643 <SCH>
A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1048 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF----GHENSW
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,332,817,965,1017,1333,1616,1626/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 15.9%; Score 177; DB 2; Similarity 31.5%; Pred. No. 2.1e-07; 45; Conservative 17; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                     -----RWNDVPCNYNLPYVCK 1161
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                                            188
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(Species: Mus musculus (house mouse)
(C,Species: Mus musculus (house mouse)
(C,Species: Mus musculus (house mouse)
(C,Accession: A48925; 321320; PC2245
(C,Accession: A48925; 321320; PC2245
(C,Accession: A48925; 321320; PC2245
(C,Accession: A48925; 321320; PC2245
(C,Accession: A48925; Mulp:93043353; PMID:1421407
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(C,Accession: A48925; Mulp:93043353; PMID:1421407
(C,Accession: A48925; Mulp:93043353; PMID:1421407
(C,Accession: A48925; Mulp:93043353; PMID:1421407
(C,Accession: A48925; Mulp:93043353; PMID:1421407
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(C,Accession: A58925; Mulp:93043353; PMID:1421407
(C,Accession: A48925; PMID:142140; PMID:1421407
(C,Accession: A48925; PMID:1421407
(C,Accession: A489
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A/Status: preliminary
A/Status: preliminary
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Cossareferences: EMBL:Z11974; NID:952997; PIDN:CAA78028.1; PID:952998
B/Charris, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Super
Biochem: Biophys. Res. Commun. 198, 682-692, 1994
A/FILL: The exon-intron structure and chronosomal localization of the mouse macrophage
A/Reference number: PC2245; MUD:94128116; PMID:8297379
A/Residues: 35-105 cHA3>
C/Genetics:
A/Residues: 35-105 cHA3>
A/Map position: 2
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                                                                                                                                                    81 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY
                                                                                                                                                                                                                                                     139 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE-----
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llarity 25.9%; Pred. No. 1.8e-07;
Conservative 33; Mismatches 66
                                                                                                                                                                                                                                                                                                      ----WDINCGYPNAFICQRHNSSINATTVMP----
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J. Biol. Chem. 270, 958-965, 1995
Afitle: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan general A; Reference number: A55535; MUID:95122551; PMID:7822336
A; Accession: A55535
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;21-257/Product: neurocan #status predicted <NAT>
F;23-1257/Product: neurocan #status predicted <NAT>
F;216-253/Domain: link protein repeat homology <LNK1>
F;214-355/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-G-D) motif
F;353-984/Domain: cell attachment (R-G-D) motif
F;323-984/Domain: C-type lectin homology <LCH>
F;1029-1149/Domain: C-mplement factor H repeat homology <FHD>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;1156-1313/Pomain: complement factor H repeat homology sele: carbohydrate (Ser) (covalent) #status predicted
F;372,410/Rainding site: chondroitin sulfate (Ser) (covalent) #status experimental
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C.Species: Mus musculus (house mouse)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: AS5335
R.Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
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30.8%; Pred. No. 3.9e-07;
tive 18; Mismatches 49;
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Best Local Similarity 28.5%; Pred. No. 8.3e-07;
Matches 47; Conservative 23; Mismatches 55;
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A.Molecule type: mRNA
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R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
B;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine braintacrence number: Z17954; MUID:98288320; PMID:9624174
A;Accession: T42389
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C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggrega
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; C;Keywords: chondroitin sulfate proteoglycan; glycoprotein
                                                                                                                                                                                                                                                                                               11;
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                                                           131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       versican precursor, splice form VO - bovine
N;Alternate names: chondroitin sulfate proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
                                                 76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3210 WIGL------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG--
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                                                                                                                                                                                                                                        132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE---
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Best Local Similarity
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40;

55; Indels

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F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
                                                                                                                            F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                      ch 15.6%; Score 174; DB 1; Similarity 28.5%; Pred. No. 8.3e-07; 47; Conservative 23; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 28.54 Matches 47; Conservative
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A, Residues: 1-3562 <SHI>
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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J. Biol. Chem. 267, 23883-23887, 1992
J. Biol. Chem. 267, 23883-23887, 1992
A; Title: Isolation of a large aggregating proteoglycan from human brain.
A; Reference number: A45131; MUID:93054750; PMID:1429726
A; Contents: brain
A; Molecule type: protein
A; Residues: 21-22, X', 24-37 < PE2>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:118884)
B; Note: sequence extracted from NCBI backbone (NCBIP:118884)
B; Note: sequence extracted from NCBI backbone (NCBIP:118884)
B; Note: sequence extracted from NCBI backbone (NCBIP:118884)
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:118884)
B; Note: sequence extracted from GB/EMBL/DDBJ
A; Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chrow in the seature in the sequence of SE32488; NID:92633313; PIDN:AAB24878.1; PID:92633314
A; Status: translated from GB/EMBL/DDBJ
A; Cross-references: GBS:52488; NID:92633313; PIDN:AAB24878.1; PID:92633314
A; Cross-references: GBB:127873; OMIM:118661
A; Map postition: 5q12-5q14
C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology; A; Nama postition: signal sequence #status predicted csIG>
F; 1-20/Domain: signal sequence #status predicted csIG>
F; 1-20/Domain: signal sequence #status predicted csIG>
F; 1-21-2409/Product: proteoglycan 24K core protein #status predicted csIG>
F; 1-21-2409/Product: proteoglycan 24K core protein #status predicted csIG>
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                                                                                                                            versican precursor - human
NyAlternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
NyAlternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
NyAlternate names: chordroitin sulfate proteon
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S06014; S43921, A60979; A30358; A29348; A45131; I54179
R;Zimmermann, D.R; Ruoslahti, E.
R;Zimmermann, D.R; Ruoslahti, E.
A;Title: Multiple domains of the large fibroblast proteoglycan, versican.
A;Reference number: S06014; MUID: 90059882; PMID: 2583089
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Anolecule: type: protein

A; Molecule: 24-50;80-87,'D', 89-119;128-155;167-218;229-259,'IR';261-268;277-283,'G',285-

R; Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.

B; Biol. Chem. 262, 13120-13125, 1987

A; Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like

A; Reference number: A29348; MUID:88007514; PMID:2820964
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A;Residues: 171-210;289-303 <BIG>
R;Perides: G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. (;hem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2466833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Structural similarity of hyaluronate binding proteins in brain and cartilage. A;Reference number: A60979; MUID:89229983; PMID:2469524 A;Accession: A60979
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A; Molecule type: mRNA
A; Residues: 1-2409 <21N5
A; Cross-references: GB: X15998; NID: G37662; PIDN: CAA34128.1; PID: G37663
A; Cross-references: GB: X15998; NID: Might, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
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A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Bignami, A; Lane, W.S; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
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A;Residues: 1725, V, 1727-2409 <KRU>
A;Cross-references: GB:J02814
R;Perides, G.; Rahemtulla, F.; Lane,
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chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed durin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A; Experimental source: stage 22-23 developing limb buds
A; Note: sequence extracted from NCBL backbone (NCBIN:134456, NCBIP:134457)
C; Superfamily: chicken chondroitin sulfate protecglycan PG-M core protein; C-type lecti
F; 166-243/Domain: link protein repeat homology <LNK1>
F; 244-345/Domain: link protein repeat homology <LNK2>
F; 328-3289/Domain: EGF homology <EGFP>
F; 3296-3327/Domain: EGF homology <EGFP>
                                              2190 QGQCYK--YF---AHRRTWDAAERECKLQGAHLTSILSHEEQMFVNRV-----GHDYQ 2237
                                                                                                                                                                                                           2238 WIGL------NDKMPEHDFRWIDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 WIGLRRREEKOSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDBQKLIEKFIENLLPSDGDF- 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                             -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTPGK 3475
                                                                                                                                                                                                                                                                                                                          132 AGIGGPYMPQWNDDRCNMKNNPICKYS----DEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;3334-3454/Domain: C-type lectin homology <LCH>F;3461-3517/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A47171; MUID:93300846; PMID:8314802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 171; DB 2; 28.5%; Pred. No. 2.4e-06; iive 23; Mismatches 55.
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A Accession: E29164
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1230-1249 < PE2.
C; Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; 1
C; Keywords: glycoprotein
C; Keywords: glycoprotein
F; 89-28/Domain: link protein repeat homology (fragment) < LNK1>
F; 29-58/Domain: link protein repeat homology (fragment) < LNK2>
F; 80-146/Domain: link protein repeat homology (fragment) < LNK3>
F; 167-28/Domain: link protein repeat homology (LNK4>
F; 167-28/Domain: link protein repeat homology < LNK4>
F; 1130-1250/Domain: C-type lectin homology < LCH>
F; 1130-1250/Domain: complement factor H repeat homology < FHD>
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A,Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; I
C;Keywords: cartilage; chondroltin sulfate proteoglycan; extracellular matrix; glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggrecan precursor, cartilage long splice form [validated] - human NyAlternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; N;Contains: aggrecan cartilage short splice form c;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42610
R;Hering, T.M.; Kollar, J.; Huynh, T.D.
A;Description: Complete coding sequence of bovine aggrecan: comparative structural A;Reference number: Z22182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1178 NN---NAQDYQWIGL------NDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1127 ÖKLCEEGWTKFQGHCYR--HFPD---RATWVDAESQCRKQQSHLSSIVTPEEQ----EFV 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2165 NN---NAODYOWIGL-----NDKTIEGDFRWSDGHSLOFENWRPNOPDNFFATGEDC 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 VVMIWHEKG------EWNDVPCNYQLPFICKKGTVACGEPPVVEHARIFGOKKD 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 QPVCRGG---TQRPCYKVIYFHDTSRRLNFBEAKBACRRDGGQLVSIESEDEQKLIEKFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                  A; Reference number: A91327; MUID: 85027710; PMID: 6489519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.2%; Score 158.5; DB 2
Best Local Similarity 26.8%; Pred. No. 9.9e-06;
Matches 48; Conservative 29; Mismatches 59
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A;Molecule type: mRNA
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Best Local Similarity
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R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomen
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A;Status: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: protein
A;Residues: 1-28;59-82;131-137,'08ET',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
B;Perin, J.P.; Bonnet, F.; Jolles, P.
A;Perin, J.P.; Bonnet, F.; Jolles, P.
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: Large type: MRNA
A;Molecule type: Large type: MRNA
A;Cross-references: GB:J05028
B;Oldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from A;Reference number: A27752; MUID:87270630; PMID:3111460
A;Accession: A27752
C;Accession: T42710

R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Basky, L.A.
J. Lasky, L.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFEPNFRDSLEDCVT 482
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A;Molecule type: mRNA
A;Residues: 622-1340 <0LD>
A;Residues: 622-1340 <0LD>
B;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by
A;Reference number: A39808; MUID:91217051; PMID:2022637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1479;
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15.3%; Score 170.5; DB 2; Length 1.
Best Local Similarity 31.4%; Pred. No. 9.6e-07;
Matches 48; Conservative 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteoglycan core protein, cartilage - bovine (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 156
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Fig. 247. Domain: link protein repeat homology <LNK2>
Fig. 249. Sp. 247. Domain: link protein repeat homology <LNK2>
Fig. 249. Sp. 247. Domain: link protein repeat homology <LNK3>
Fig. 249. Sp. 247. Domain: link protein repeat homology <LNK3>
Fig. 240. Sp. 247. Domain: link protein repeat homology <LNK3>
Fig. 240. Sp. 247. Domain: link protein repeat homology <LNK3>
Fig. 240. Sp. 247. Domain: chondroitin sulfate attachment #status predicted <CS1>
Fig. 240. Sp. 248. Domain: Condition sulfate attachment #status predicted <CS2>
Fig. 240. Sp. 248. Domain: Complement factor H repeat homology <FHD>
Fig. 240. Sp. 249. 
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C;Species: Au Amar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: S23174; B42755
R;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
R;Becker-Andre, 206, 401-411, 1992
A;Title: Murine endochelial leukccyte-adhesion molecule 1 is a close structural and fun A;Reference number: S23174; MUID:92283265; PMID:1375914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
B;Weller, A.; Isenmann, S.; Vestweber, D.
B;Weller, A.; Isenmann, S.; Vestweber, D.
A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-select
A;Reference number: A42755; MUID:92340571; PMID:1378846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109470)
A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PID:g
A;Note: it is uncertain whether the initiator is Met-1 or the AUG codon preceding that C;Superfamily: P-selectin, C-type lectin homology; complement factor H repeat homology; C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2202 QEVCEEGWNKYQGHCYR--HFPD---RETWVDAERRCREQQSHLSSIVTPEEQ----EFV 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2253 NN---NAQDYQWIGL-----NDRTIEGDFRWSDGHPMQFENWRPNQPDNFFAAGEDC 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2302 VVMIWHEKG------EWNDVPCNYHLPFTCKKGTVACGEPPVVEHARTFGOKKD 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-selectin precursor - mouse N/Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown
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A;Molecule type: protein
A;Ratus: preliminary
A;Molecule type: protein
A;Ratus: preliminary
Bjochem. J. 313, 933-940, 1996
A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Reference number: S62786
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Reference number: S62786; MUID:930248; PIDN:CA35463.1; PID:930249
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162,2201-2415 <DUD>
A;Residues: 1778-1927, A',1929-1963, V',1965-2162, 2201-2415 <DUD>
A;Reference the nucleotide sequence was submitted to the EMBL Data Library, January 1990
B;Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
J. Biol. Chem. 264, 15747-15750, 1989
A;Title: A new epidermal growth factor-like domain in the human core protein for the lar A;Reference number: A34226
A;Reference number: A34226
A;Rocession: A34226
A;Ro
                                            R. Poege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
J. Biol. Chem. 266, 894-902, 1991
A,Title: Complete coding sequence and deduced primary structure of the human cartilage layerence number: A39086; MUID:91093289; PMID:1985970
A,Accession: A39086
A,Reference number: A39086; MUID:91093289; PMID:1985970
A,Residues: 1-2162,2201-2329,'A',2392-2415 <DE>
A,Cross-references: GB:MS5712; NID:91708258; PIDN:AA62824.1; PID:9178259
A,Residues: 1-2162,2201-2329,'A',2392-2415 <DE>
A,Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by A,Reference number: S50206; MUID:95035091; PMID:7524681
A,Accession: S50206
A,Reterences: EMBL:X80278; NID:9516295
A,Residues: 350-497 <GLU>
A,Residues: 350-497 <GLU>
A,Residues: 350-497 <GLU>
A,Residues: 350-497 <GLU>
A,Residues: 350-497 <GLU>
A,Residues: 350-497 <GLU>
A,Title: Analysis of aggrecan fragments in human synovial fluid. Evidence for the interval in the structure of aggrecan fragments in human synovial fluid. Evidence for the interval in the structure of aggrecan fragments in human synovial fluid.
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A, Molecule type: protein
A, Residues: 361-370, X7, 372-373,393-399, X7, 401-407, X7, 409 <SAN>
A; Residues: 361-370, X7, 372-373,393-399, X7, 401-407, X7, 409 <SAN>
A; Cross-references: PIDN:AAB22079.1; PID:g248844; PIDN:AAB22077.1; PID:g248842; PIDN:AAB
A; Experimental source: synovial fluid
A; Experimental source: synovial fluid
A; Note: sequences modified after extraction from NCBI backbone
B; Barry, F. P.; Neame, P. J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A; Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
A; Reference number: 146998; MUID:95128522; PMID:7827755
A; Molecule type: DNA
       C43
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A.Residues: 764-765, 47, 767-846, 7V, 848-862, 7X, 864 cBAR>
A.Kesidues: 764-765, 47, 767-846, 7V, 848-862, 7X, 864 cBAR>
A.Kross-references: EMBL:874659; NID:9807127; PIDN:AAG60643.1; PID:9807128
A.Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue R.Hilic, M.Z.; Mox, M.T.; Milliamson, 0.0D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
A.Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the A.Accession: S66389; MUID:96004775; PMID:7574678
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                                                                                                                                                                                                                    cartilage
       C,Accession: A39086; S50206; A43919; S46659; S66389; S68646; S62786; A34226; B43919;
R;Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
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A;Nolecule type: protein
A;Rolecule type: protein
R;Residues: 17-23:24' X',26-27;393-401;402-403 <ILI>
R;Residues: 17-23:24' X', Knaeuper, V.; Murphy, G.; Neame, P.J.
R;Rosang, A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
R;Rosang, Lett. 380, 17-20, 1996
A;Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13)
A;Reference number: S68646; MUID:96181659; PMID:8603731
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A;Remiduem: 1936-1963,'V',1965-2069,'A',2071-2415 <BAL>
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Cispeciaes Rattus norvegicus (Norway rat)
Cispeciaes Rattus norvegicus (Norway rat)
Cipacession: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
CiAccession: A92623, A23835, A28453, A28095, A28452
Riboege, K.; Sasaki, W.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deducate number: A92623; MUID:88087070; PMID:3693370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA Apples 1856-2124 (ADD2)
A; Mesidues: 1856-2124 (ADD2)
A; Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
B; Neame, P.J.; Christner, J.E.; Baker, J.R.
B; Blol. Chem. 262, 17768-17778 1987
A; Title: Cartilage protecoglycan aggregates. The link protein and protecoglycan amino-term A; Reference number: A28453; MUID:88087071; PMID:3693371
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A; Residues: 20-37, W',39-60, E',62-64, X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A',
A; Residues: 20-37, W',39-60, E',62-64, X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A',
C; Superfamily: aggreean: C-type lectin homology; Complement factor H repeat homology; EC
C; Reywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <NAT>
F;10-124/Product: proteoglycan core protein #status predicted <NAT>
F;44-135/Domain: immunoglobulin homology <LNK1>
F;170-247/Domain: link protein repeat homology <LNK2>
F;568-349/Domain: link protein repeat homology <LNK3>
F;568-340/Domain: link protein repeat homology <LNK4>
F;504-581/Domain: link protein repeat homology <LNK4>
F;504-583/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;2041-2097/Domain: complement factor H repeat homology <FHD>
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A; Residues: 1-2124 *CDC5-
R; Doege, K; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
B. Biol. Chem. 263, 10040a, 1988
A; Reference number: A30069
A; Contents: annotation; revision to residue 698
R; Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A; Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat A; Reference number: A23835; MUID:86250698; PMID:2424893
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: P-selectin #status predicted <MAT>
F;22-612/Product: P-selectin #status predicted <MAT>
F;143-174/Domain: EGF homology <EGF>
F;143-174/Domain: complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;36-363/Domain: complement factor H repeat homology <FH3>
F;36-426/Domain: complement factor H repeat homology <FH3>
F;36-448/Domain: complement factor H repeat homology <FH6>
F;31-489/Domain: complement factor H repeat homology <FH6>
F;35-391,528/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 YYNASSELMTYDEASAYCQRDYTHLVAIQNKEE---INYLNSNLKHSPSYYMIGIRK---
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Best Local Similarity 27.99
Matches 38; Conservative
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F;126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status pre
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                                                                                                                                                                        9 QPVCRGG---TQRPCYKVIYFHDTSRRLNPEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                        Gaps
                                                                                                                  Indels 43;
                                                               Length 2124;
                                                         DB 2;
                                                                                                                  62;
                                                         Query Match
13.8%; Score 153.5; DB 2
Best Local Similarity 26.3%; Pred. No. 4.7e-05;
Matches 47; Conservative 27; Mismatches 62
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completed: December 22, 2003, 16:14:40 e : 10.0151 secs

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61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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Patent No. US20020058310A1;
GENERAL INFORMATION;
APPLICANT: Immunex Corporation;
APPLICANT: Anderson, Dirk M;
ITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES;
CURRENT APPLICATION NUMBER: US/09/887,855;
CURRENT FILING DATE: 2001-06-22;
NUMBER: PatentIn version 3.1;
SOFTWARE: PatentIn version 3.1;
SEQ ID NO.5;
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 100.0%; Score 1115; DB 9; al Similarity 100.0%; Pred. No. 7.7e-105; 206; Conservative 0; Mismatches 0;
US-09-907-942-137
US-09-904-859-137
US-09-904-820-137
US-09-904-786-137
US-09-906-7646-137
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US-09-906-700-137
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US-09-905-811-137
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US-09-905-075-137
US-09-902-775-137
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   ORGANISM: Homo sapiens
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Matches 206; Conserv
   RESULT 1
US-09-887-855-5
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1115
1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-094-749-2142
US-09-909-0888-137
US-09-905-291A-137
US-09-905-291A-137
US-09-907-824-137
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2090
LENGTH: 374
NUMBER OF SEQ ID NOS: 3381
                                                                                      ; ORGANISM: Homo sapiens
US-10-094-749-2090
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ORGANISM: Homo sapiens
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                                                                                                                 APPLICANT: Immunex Corporation
APPLICANT: Anderson, Dirk M
TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
FILE REPRENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
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Publication No. US20030219741A1
                                                               Sequence 2, Application US/09887855
Patent No. US20020058310A1
GENERAL INFORMATION:
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOYO, JUN-ICHI
ISONO, YUUKO
HIO, YUUKI
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OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOM
                                                                                                                                                                                                                                                                                       LENGTH: 374
TYPE: PRT
CRGANISM: Homo sapiens
US-09-887-855-2
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61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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APPLICANT: YUE, Henry
APPLICANT: AZIMAL, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LAL, Provi
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     Length 374;
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// OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1

US-10-149-819-15
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Query Match
100.0%; Score 1115; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.7e-104;
Matches 206; Conservative 0; Mismatches 0;
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100.0%; Score 1115; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-104;
Matches 206; Conservative 0; Mismatches 0;
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04

PRIOR PELICATION NUMBER: US/01/3,048

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerriteen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Mather, Jennie P.
                                                             Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
121 CVVMYHQPSAPAGIGGPYMPQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                    61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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Best Local Similarity 99.5%; Pred. No. 4.4e-104;
Matches 205; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIVE, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: HO, YUUKO
APPLICANT: HO, YUKRO
APPLICANT: HIS, KYOTARO
APPLICANT: NAGAI, KEIICHI
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TOSUKA, MACHYKO
APPLICANT: TOSUKA, MACHYKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: MASUHO, YASUHIKO
TITLE REFERENCE: 084335,0160
CURRENT APPLICATION NUMBER: 08/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                                                   202 LPEETQEEDAKKTFKESREAALNLAY 227
                                                                                                                  181 LPEETQEEDAKKTFKESREAALNLAY 206
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Publication No. US20030219741A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
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RESULT 6 US-09-909-320-137 ; Sequence 137, Application US/09909320

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96.3%; Pred. No. 4.6e-103;
ive 0; Mismatches 0;
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-06
PRIOR PRIOR DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-07
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Mather, Jennie P.
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APPLICANT: Ashkenai, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 96.3'
Matches 206; Conservative
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CORGANISM: Homo sapiens
US-09-909-088B-137
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                                                                                                                                                                                                                                                                                                                                                    142 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGE 201
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                                                                                                                                                22 ATGRILSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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                                                                                                                  1 ATGRILS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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                                                                 Gaps
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        Length 382;
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al Similarity 96.3%; Pred. No. 4.6e-103;
206; Conservative 0; Mismatches 0;
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembz
TITLE OF INVENTION: Acids Encoding the Sam
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909, 088B
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1990-02-22
PRIOR PELING DATE: 1990-07-07
PRIOR PELING DATE: 1990-07-07
PRIOR PLING DATE: 1990-07-26
PRIOR PLING DATE: 1990-07-26
PRIOR PLING DATE: 1990-07-28
PRIOR PLING DATE: 1990-09-08
PRIOR PLING DATE: 1990-09-08
PRIOR PELING DATE: 1990-09-08
PRIOR PELING DATE: 1990-09-13
PRIOR PELING DATE: 1990-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Patent No. US20020146709A1
GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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        Query Match
Best Local Similarity
Matches 206; Conserv
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APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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CURRENT PAPLICATION NUMBER: US/09/02, 853

CURRENT PILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-09-18

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

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PRIOR PILING DATE: 1999-09-15

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PRIOR PILING DATE: 1999-10-05

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PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 199
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Paoni, Nicholas F
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Gerber, Hanspeter
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Mather, Jennie P.
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                            GENERAL INFORMATION:
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APPLICANT:
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ORGANISM:
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APPLICANT: Williams, P. Mickey
APPLICANT: Worliams, P. Mickey
APPLICANT: Wood, william, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
FULB REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US/09/905,291A
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLILNG DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLILNG DATE: 1999-07-08
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PRIOR PLILNG DATE: 1999-09-08
PRIOR PLILNG DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/2809
PRIOR PLILNG DATE: 1999-10-05
PRIOR PLILNG DATE: 1999-10-05
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; ORGANISM: Homo sapiens
US-09-905-291A-137
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US-09-902-853-137
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53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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Best Local Similarity 96.3%; Pred. No. 4.6e-103;
Matches 206; Conservative 0; Mismatches 0;
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                  PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1090-12-07

PRIOR PLING DATE: 2000-01-05

NUMBER: PCT/USOU/00219

PRIOR PLING DATE: 2000-01-05

    APPLICATION NUMBER: PCT/US99/23089
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-09-907-824-137
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US-09-907-841-137
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                                                                                                                           81
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBRUE: 10466-14
CURRENT APPLICATION UMBER: US/09/907,824
                                                                                                                                                                                                      ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD
                                                                                                            22 ATGRILSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                             1 ATGRLLS------GOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                              Gaps
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                              0; Indels
96.3%; Pred. No. 4.6e-103; tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07-08
PRIOR PELING DATE: 1999-07-06
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L
  Best Local Similarity 96.3
Matches 206; Conservative
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Gao, Wei-Qiang
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APPLICARTY WOOD, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CURRENT FILMS OF THE REPRENCE: 10466-1.

CURRENT FILMS OF THE 2010-01-11

PRIOR APPLICATION NUMBER: US/09/04.011

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PLILNG DATE: 1999-07-26

PRIOR PLILNG DATE: 1999-07-28

PRIOR PLILNG DATE: 1999-07-28

PRIOR PLILNG DATE: 1999-09-06

PRIOR PLILNG DATE: 1999-09-08

PRIOR PLILNG DATE: 1999-09-08

PRIOR PLILNG DATE: 1999-09-13

PRIOR PLILNG DATE: 1999-09-13

PRIOR PLILNG DATE: 1999-09-13

PRIOR PLILNG DATE: 1999-09-13

PRIOR PLILNG DATE: 1999-10-12

PRIOR PLILNG DATE: 1999-10-12

PRIOR PLILNG DATE: 1999-10-13

PRIOR PLILNG DATE: 1999-10-12

PRIOR PLILNG DATE: 1999-10-12

PRIOR PLILNG DATE: 1999-11-20

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR APPLICATION NUMBER: PCT/US99/20911

PRIOR APPLICATION NUMBER: PCT/US99/20911

PRIOR APPLICATION NUMBER: PCT/US99/20911

PRIOR APPLICATION NUMBER: PCT/US99/30099

PRIOR PLILNG DATE: 1999-11-20

PRIOR APPLICATION NUMBER: PCT/US99/30099

PRIOR PLILNG DATE: 1999-12-20

PRIOR PLILNG D
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Pred. No. 4.6e-103;
0; Mismatches 0;
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                       Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Williams, P. Mickey
Wood, William, I.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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                                                                                                                                     Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 96.3
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-137
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PRILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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22 ATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFBEAKEACRRDGGQLVSI
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5. US20030003530A1
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bersoyers, Luc
APPLICANT: Bersoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
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Gerritsen, Mary E
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Best Local Similarity 96.3
Matches 206; Conservative
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Gao, Wei-Qiang
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US-09-907-841-137
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US-09-904-011-137
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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98.7%; Score 1101; DB 11;
Best Local Similarity 96.3%; Pred. No. 4.6e-103;
Matches 206; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 2090-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
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CURRENT APPLICATION NUMBER: US/09/906, 838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 137, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                US-09-906-742-137
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                           EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                      RPPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
RITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
HILE OF INVENTION: Acids Encoding the Same
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                                                                                                                    173 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
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PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04114
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
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PRIOR PELING DATE: 1999-11-20
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
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PRIOR APPLICATION NUMBER: 09/665,350
                                                                                                                                                                                                                                                                                  Sequence 137, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Goddard, A.
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Mather, Jennie P.
Pan, James
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT:
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APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-17

PRICOR PELICATION NUMBER: US 60/143,048

PRICOR PELICATION NUMBER: PCT/USO0/04414

PRICOR PLING DATE: 1999-07-07

PRICOR PLING DATE: 1999-07-26

PRICOR PELICATION NUMBER: US 60/145,698

PRICOR PLING DATE: 1999-07-26

PRICOR PLING DATE: 1999-07-26

PRICOR PLING DATE: 1999-07-26

PRICOR PLING DATE: 1999-07-26

PRICOR PLING DATE: 1999-09-08

PRICOR PLING DATE: 1999-09-13

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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                  Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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Paoni, Nicholas F.
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Stewart, Timothy I
Tumas, Daniel
                               Filvaroff, Ellen
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Best Local Similarity 96.3 Matches 206; Conservative
                                                                                                                                                                                             Goddard, A.
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-06
PRIOR PLING DATE: 1999-07-26
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Publication No. US20030027145A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
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Matches 206; Conservative
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; ORGANISM: Homo Sapien
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        53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYUD 112

        Db
        82 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYUD 141

        Qy
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        Db
        142 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 201

        Qy
        173 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206

        Db
        202 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 235

        Search completed: December 22, 2003, 16:16:47

        Job time: 20.6848 sec8
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Q90xm0 mus musculu Q90xm0 pubp2 homo sapien P22897 homo sapien P52066 mus musculu Q14594 homo sapien P55067 rattus morv Q56259 mus musculu P13611 homo sapien Q28124 cantus norv Q5053 gallus gall phomo sapien Q28137 canis famil Q00690 mus musculu Q28133 canis famil Q00690 mus musculu Q39xp1 trimeresuru P07897 rattus norv Q28052 bom sapien Q28052 bom sapien Q28052 mus musculu Q39xp1 trimeresuru P07897 megabalanus Q28062 bom sapien P07898 mus musculu Q61381 mus musculu Q61381 mus musculu Q61381 mus musculu Q61381 mus musculu Q61381 mus musculu P07898 gallus gall P55068 rattus norv P1346 megabalanus P07893 fattus norv P18337 mus musculu P981837 mus musculu P918337 mus musculu P518405 sattus norv
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Copyright (c) 1993 - 2003 Compugen Ltd.
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REG CHC ID	ងក	T 1 MOUSE CHOD_MOUSE	STA	STANDARD;		PRT; 273	AA.		
AC DT		Q9CXMO; Q8VI31; 28-FEB-2003 (Rel. 41, Cre 28-FEB-2003 (Rel. 41, Las 28-FEB-2003 (Rel. 41, Las	131; (Rel. (Rel. (Rel.	41, Cr 41, La 41, La	eat st s	(31) (Rel. 41, Created) (Rel. 41, Last sequence update) (Rel. 41, Last annotation updat	ê		
3 8		CHODL.	ın prec	ursor	(Tre	(Transmembrane protein	otein MT75).		
8888		Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalia; Butheria; Rodentia; NCBT TaxTh-1000.	s (Mouse) Metazoa; utheria;	t; Chor t; Rode	data ntia		Craniata, Vertebrata, Euteleosto Sciurognathi, Muridae, Murinae,	Euteleostomi Murinae; Mu	omi; Mus.
S S		UENCE FR	OM N.A.						
R RA		STRAIN-C57BL/6J; Weng L., Smits P., Hubner R., Wo "Mt75, a low expressed c-type le	L/6J; its P., w expre	Hubne	r R.	, Wouters J., Merregaert oe lectin gene involving	Merregaert J involving in		
F 된		ndrogene mitted (sis."; ocr-200	(0)	the	chondrogenesis."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases	DDBJ database	. 88	
8 8 8 5 6 5	SEQ STR	[2] SEQUENCE FROM N.A STRAIN=C578L/6.1: '	OM N.A.	TSSTE	, deg	. bead oinov			
22	MED	LINE=210	85660; hinagaw	PubMed	=112 Shib	X MEDLINE=21085660; PubMed=11217851; A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	no M., Itoh M	1., Ishii	, ,
\$ \$	Ara Aiz	ikawa T.,	Hara A Izawa M	, Fuk	unie hi x	hi Y., Konno l	H., Adachi J.	, Fukuda Yamanaka	
8 8	Sai Kad	to T., O	kazaki Matsuda	Y., Go H.A.,	Jobc	ri T., Bono H burner M., Ba	., Kasukawa 1 talov S., Cae	C., Saito	i ex
\$ \$	Fle	ischmann hl P., L	W., Ga ewis S.	asterla , Matsi	and to Y	T., Gissi C., ., Nikaido I.	King B., Koc, Pesole G.,	hiwa H., Quackenb	ush J.,
2 2 2	Sak	riml L.M	, Stau kido T.	bli F. , Furu	Su M	zuki R., Tomil I., Aono H., Ba	ta M., Wagner aldarelli R.,	L., Was Barsh G	hio T.,
\$ \$ 5	Bro	wnstein	Ottelli M.J., B	ult C.	בייור בייור	ga N., Carnin etcher C., Fu	ci P., de Bor jita M., Gari	laldo M.F. boldi M.	
8 8 8	Lys	ns P., M.	archion	ni L., ,	Mag	hima J., Mazze	arelli J., Mo	M., Lee	,
22	Sas	aki H.,	Sato K.	School	enba	Sasaki H., Sato K., Schoenbach C., Seya T., Shibat Susuki H., Tovo-oka K. Wang K H. Weitz C.	., Shibata Y., Storch K1	Storch	KF.,
RA RA		Wynshaw-Boris Havashizaki y	ie A.	Yoshida	Α.	, Hasegawa Y.,	. Kawaji H.,	Kohtsuki	S.,
	ý	nctional ure 409;	annota 585-690	tion of (2001)	κ '	"Functional annotation of a full-length mouse cDNA collection Nature 409:685-690(2001).	^	lection.	
չ Տ		-1- SUBCELLULA -1- SIMILARITY	ILAR LO	CATTON- ntains	50	LOCATION: Type I membrane protein (Pote: Contains 1 C-type lectin family domain.	protein (Pot Eamily domain	(Potential). omain.	
388		SWISS-1	PROT en	try is	d o	yright, It is	t. It is produced through a collaboration	ongh a co	ollaboratio
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388		use by nor modified and	1-prot1	t inst stateme	1 1 1	use by non-profit institutions as long amodified and this statement is not removed.	as its conte	ent is and for	B in no way for commercial
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EMBL; AF311699; AAL50354.1;

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MEDLINE=20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
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MEDLINE=22074930; PubMed=12079204;
Meng L., Smits P., Wauters J., Merregaert J.;
"Molecular cloning and characterization of human chondrolectin, a novel type I transmembrane protein homologous to C-type lectins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamm.lia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                           . .) (POTENTIAL)
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                                                                                             23 CHONDROLECTIN.
216 EXTRACELLULAR (POTENTIAL).
237 POTENTIAL.
238 CYTOPLASMIC (POTENTIAL).
179 C-TYPE LECTIN.
86 N-LINKED (GLCNAC. . .) (POTE
24 V -> W (IN REF. 2).
179 T -> K (IN REF. 2).
179 T -> K (IN REF. 2).
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                                      PERMI, PF00059, lectin c, 1...
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; CTYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS550041; C_TYPE_LECTIN 2; 1.
Lectin; Transmembrane; Glycoprotein; Signal.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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EMBL; AK014255; BAB29226.1; --
HSSP; P22897; 1EGG.
MGD; MGI:2179069; Chodl.
InterPro; IPR001304; Lectin_C.
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70 LVSIESEDEQKLIEKFIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSI 124
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.; "Primary structure of the mannose receptor contains multiple motifs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                 C-TYPE LECTIN.
N-LINKED (GLCNAC. . .) (POTENTIAL)
F4890AAFB572A311 CRC64;
                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=93052405; PubMed=1294118; Kim S.J., Ruiz N., Bezouska K., Drickamer K.; "Organization of the gene encoding the human macrophage mannose
                                                                                                                                                                      32.2%; Score 645; DB 1; Length 273; 48.4%; Pred. No. 3.6e-47; ive 40; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen)
                                                                                                                                                                                                                                                                                                                                                                            234 AFGTCCFQMLHKSKGRTKTSPN---QSTLWISKSTRKESGMEV 273
                                                                                                                                                                                                                                                                                                                                                                242 TTVVCWVWICRKRK-REOPDPSTKKOHTIWPSPHOGNSPDLEV 283
                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                       CYTOPLASMIC (POTENTIAL).
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STUDIES ON THE BINDING OF INDIVIDUAL LECTIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resembling carbohydrate-recognition domains.";
J. Biol. Chem. 265:12156-12162(1990).
             MIM; 607247; -...
InterPro; IPR001304; Lectin_C.
PFam; PP00059; lectin_c; 1...
PRART; SR00034; CLECT; 1...
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1...
Lectin; Transmembrane; Glycoprofein; Signal.
SIGNAL
                                                                                              CHONDROLECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1456 AA
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                                                                                                               POTENTIAL.
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MEDLINE-90324192; PubMed=2373685;
                                                                                                                                                   273 AA; 30431 MW;
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01-AUG-1991 (Rel. 19, Last seq
28-FEB-2003 (Rel. 41, Last ann
       Genew; HGNC:17807; CHODL.
                                                                                                                                                                                         Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                           "Structure of a C-type carbohydrate recognition domain from the macrophage mannose receptor.";

J. Biol. Chem. 275:21539-21548 (2000).

J. Biol. Chem. 275:21539-21548 (2000).

-!-FUNCTION: MEDIATES THE ENDOCYTOSIS OF GLYCOPROTEINS BY MACROPHAGES, IN SEVERAL RECOGNITION AND UPTAKE PROCESSES.

-!-SUBCELLULAR LOCATION: Type I membrane protein.

-!-MISCELLULAR LOCATION: Type I membrane protein.

-!-MISCELLULAR LOCATION: Type I membrane protein.

-!-MISCELLULAR ENDOCATION: Type I membrane protein.

-!-MISCELLULAR ENDOCATION: Type I membrane protein.

-!-MISCELLULAR ENDOCATION: Type I membrane protein.

-!-MINTARITY: Contains 8 C-type lectin family domains.

-!-SIMILARITY: Contains 1 rich B-type lectin domain.

-!-SIMILARITY: Contains 1 rich B-type lectin domain.

-!-MAM="http://www.ncbi.nlm.nih.gov/prow/guide/1644341555_g.htm".
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                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.
MEDLINE=20347275; PubMed=10779515;
Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
                               Taylor M.B., Bezouska K., Drickamer K.;
"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726 (1992).
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MEDLINE=92112893; PubMed=1730714;
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PDB; 1EGI; 30-AUG-00.
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         Conterpro; IPR002353; Antifreeded endocytosis; TAS.

Refero; IPR002553; Antifreeded.

Refero; IPR000362; FN Type II.

Refero; IPR000372; Ricin_B_lectin_C.

Refero; IPR00372; Ricin_B_lectin_C.

Refero; PR00359; Ricin_B_lectin, 2.

Refero; PR00359; Ricin_B_lectin; 2.

RINTS; PR00039; FNTYPEII.

REFEROSES: RICIN_C.

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FIRROMCTIN TYPE-II.
C-TYPE LECTIN 1 (LONG FORM).
C-TYPE LECTIN 3 (LONG FORM).
C-TYPE LECTIN 4 (LONG FORM).
C-TYPE LECTIN 5 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
C-TYPE LECTIN 6 (LONG FORM).
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                                                                                                                102 RREEKOSNSTACODLYAWIDGSISOFRNWYVDEPSCGS--EVCVVMYHOPSAPAGIGGPY 159
                                                                                                                                                                                                                                                                                          "Structure and chromosomal localization of the mouse neurocan gene."; Genomics 28:405-410(1995).

-!- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic acid.
                                                                                                                                                                                                                                                                160 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETOE----
                                                                                                                                                                                                       Gaps
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
CSPG3 OR NCAN.
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                             54;
    Length 1456;
                                             66; Indels
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MEDLINE=96039250; PubMed=1490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.
Faessler R.;
Query Match 9.2%; Score 183; DB 1; Best Local Similarity 25.1%; Pred. No. 3.8e-07; Matches 53; Conservative 38; Mismatches 66
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PIR; S52781; S52781.
HSSP, P00740; 1EDM.
MGD; MGI:104664; Cspg3.
InterPro; IPR001353; Antifreezell.
InterPro; IPR00155; Asx hydroxyl.
InterPro; IPR00163; EGF_2.
InterPro; IPR001891; EGF_Ca.
InterPro; IPR001801; EGF_Ca.
InterPro; IPR00110; IGF Ca.
InterPro; IPR00110; IGF Ca.
InterPro; IPR00110; IGF Ike.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR0000436; Sushi_SCR_CCP.
Pfam; PP00008; EGF; 2.
Pfam; PP00007; ig; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
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SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 2 Link domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                014594; Q9UPK6;
28-FEB-2003 [Rel. 41, Created)
28-FEB-2003 [Rel. 41, Last sequence update)
15-SEP-2003 [Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
CSPG3 OR NCAN OR NEUR.
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Lamerdin J.B., McCready P.M., Skowronski B., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyla A., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Kyla A., Ramirez M., Stilwagen S.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.
Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of an -1 Mb region containing the MEF2B gene in
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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PRT; 1321 AA
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InterPro; IPR001841; EGF_2.
InterPro; IPR001841; EGF_Ca.
InterPro; IPR001801; EGF_like.
InterPro; IPR003509; EGF_like.
InterPro; IPR003509; IG.
InterPro; IPR003101; IG.
InterPro; IPR001304; Loctin_C.
InterPro; IPR0001304; Loctin_C.
InterPro; IPR0001304; Loctin_C.
InterPro; IPR0001304; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF026547; AAC80576.1; -. BMBL, AC003110; AAB86655.1; -. BMBL, AC005244; AAC25581.1; -. HSSP, P00740; LEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00059; lectin_c; 1.
PF00084; sushi; 1.
PF00193; Xlink; 2.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:2465; CSPG3.
                                                                                                                                                                                                                                                                                                           Gene 221:199-205(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 2.
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 600826; -.
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1075:248-258(1991).

-!- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB SPECIFICITY: Cerebral white matter. Vo and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; the major isoform v2 is restricted to the central nervous system.

DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                     Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H., Zimmermann D.R., Zimmermann D.R., Werstcan V2 is a major extracellular matrix component of the mature bovine brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spinal cord;
MEDINE=29205262; PubMed=1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein with hyaluronic
                                                                         Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
  (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SÜBUNIT: Interacts with FBLN1 (By similarity).
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=4; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P81282-3; Sequence=VSP_003080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P81282-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 273:15758-15764(1998).
                                                                                                                                                                                                                                                     TISSUE=Forebrain;
MEDLINE=98288320; Pubmed=9624174;
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InterPro; 1PR000152; Asx hydroxyl.
InterPro; 1PR000742; EGF 2.
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EMBL, AF060458; AAC24360.1; --
EMBL, AF060459; AAC24361.1; --
PIR; T14274; T14274.
PIR; T42389; T42389.
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                                                                                                                                                                          NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=V3;
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  1145 IGLNDRIVERD-----FOWTDNTGLOFENWRENOPDNFFAGGEDCVVMVAHESG--- 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1096 QGHCYR--YF---AHRRAWEDAEKDCRRRSGHLTSVHSPEEHSFINSF-----GHENTW
                                                                                                                                                                                                    PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01181; IGF_CA; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.

EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
SUSHI.
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(POTENTIAL).
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P81282, 077669; 077610; 077611; 077612;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **Match 8.8*; Score 176; DB'1; Length 1321; Local Similarity 31.5*; Pred. No. 1.3e-06; les 45; Conservative 18; Mismatches 48; Indels 3:
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-> A (IN REF. 2).
-> R (IN REF. 2).
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               PRODOM; PD000918; Link; 2.
SWART; SW00032; CCP; 1.
SWART; SW00034; CLECT; 1.
SWART; SW000179; EGF CA; 1.
SWART; SW00409; IG_ 1.
SWART; SW00409; IG_ 1.
PROSITE; PS00010; ASX HVDROXYL; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00614; C_TYPE_LECTIN_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
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PRINTS; PR01265; LINKMODULE
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1321 AA;
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3210 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG-- 3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 3310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 WIGLRRREEKOSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
(425 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult core glycoprotein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-----
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STRAIN=Sprague-Dawley, TISSUE=Brain;
MEDLIRE=92406907; PubMed=1124557;
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
U. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                                       P -> R (in isoform V1 and isoform V3) /FT1d=VSP_003078.
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          (POTENTIAL)
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(FTd=VSP 003079.

1337 3074 Missing (In isoform V2).

(FTTd=VSP 003080.

350 3074 Missing (In isoform V3).

(FTTd=VSP 003081.

25 25 MISSING (IN REF. 2).

51 51 MISSING (IN REF. 2).

89 89 N -> D (IN REF. 2).

96 96 Q -> D (IN REF. 2).

346 346 C -> R (IN REF. 2).

3481 AA; 369984 MW; F09716FA7778D459 CRC64;
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Best Local Similarity 25.5%; Pred. No. 6.2e-06;
Matches 59; Conservative 26; Mismatches 71
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MEDLINE=94230574; PubMed=7513709;
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          NCBI_TaxID=10116;
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C-TYPE LECTIN.
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InterPro; IPR001881; EGF Ca.
InterPro; IPR005209; EGF like.
InterPro; IPR003110; Ig-Iike.
InterPro; IPR003599; Ig-
InterPro; IPR001306; Ig-MHC.
InterPro; IPR001306; Lectin_C.
InterPro; IPR001308; Like.
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R SWART; SM000918; Link; 2.

R SWART; SM000918; Link; 2.

R SWART; SM000918; Link; 2.

R SWART; SM00409; IG; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00118; EGF 2; 1.

R PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS01187; EGF 2; 1.

R PROSITE; PS01241; LINK; 2.

R PROSITE; PS01241; LINK; 2.

M Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; M EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
Margolis R.U., Grumet M.;
"The neuronal chondroitin sulfate proteoglycan neurocan binds to the
neural cell adhesion molecules Ng-CAM/L1/NILE and N-CAM, and inhibits
neuronal adhesion and neurite outgrowth.";
J. Cell Biol. 125:669-680(1994).
-:-FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                  TISSUE SPECIFICITY: EARLY POSTWATAL AND ADULT BRAIN; NOT EXPRESSED
                                                                                                                          NEUROCAN CORE PROTEIN.
150 kDa ADULT CORE GLYCOPROTEIN.
IG-LIKE V-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                            HESP, P00740; 1EDM.
INCEPPO; IPR00135; AntifreezeII.
INCEPPO; IPR00135; AntifreezeII.
INCEPPO; IPR001035; AntifreezeII.
INCEPPO; IPR001042; EGF 2.
INCEPPO; IPR001081; EGF Ca.
INCEPPO; IPR00109; EGF like.
INCEPPO; IPR001599; IGF INC.
INCEPPO; IPR001099; IGF INC.
INCEPPO; IPR001010; IGF INC.
INCEPPO; IPR001014; Lectin C.
INCEPPO; IPR001014; Lectin C.
INCEPPO; IPR000134; Link.
INCEPPO; IPR000145; Sushi_SCR_CCP.
PEam; PP00008; EGF; 2.
PEam; PP00008; IGC; 1.
PEam; PP00008; IGC; 1.
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Pfam; PF00193; Xlink; 2.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR00356; ANTIFREEZEII.
ProDom; PD000918; Link; 2.
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1037 QHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1085
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                                              EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE=98308094; PubMed=9642104;
Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
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OPERB4; 008592; 008564; OSRIK4;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

(Created)

16-OCT-2001 (Rel. 42, Last annotation update)

16-OCT-2001 (Rel. 42, Last annotation update)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 174; DB 1; Length 1257; 0.8%; Pred. No. 1.8e-06; ve 18; Mismatches 49; Indels 3:
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"Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
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                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2535-2738 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
"Molecular cloning and characterization of two developmentally regulated genes in rat lung.";
Submitted (SEP-2000) to the EMBL/Genank/DDBJ databases.
-!- FUNCTION: May play a role in intercellular matrix. May take part in the regulation of cell with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By Similarity).

-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
Margolis R.K., Margolis R.U., "Differential regulation of expression of hyaluronan-binding proteoglycans in developing brain: aggrecan, versican, neurocan, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOIG=09ERB4-3; Sequence=VSP 003092;
TISSUE SPECIFICITY: In kidney is expressed in the papillary area, but not in glomeruli.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                   ., Romer J.;
                                                                                                                                                                                                                 Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S. "Proteoglycan expression in the normal rat kidney."; Nephron 77:461-470(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
                                                                                                  Biochem. Biophys. Res. Commun. 247:207-212(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment=Additional isoforms seem to exist;
                                                                                                                                            SEQUENCE OF 2421-2463 FROM N.A. (ISOFORM VO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9ERB4-2; Sequence=VSP_003091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9ERB4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AP0308454; AAA048541; --
EMBL, AP072892; AAC26116.1; --
EMBL, AY007699; AAC16631.1; --
HSSP; PO1132; 1EPG;
InterPro; IPR000152; AEX_hydroxyl.
InterPro; IPR000152; AEX_hydroxyl.
InterPro; IPR000159; EGF_2.
InterPro; IPR000181; EGF_CA.
InterPro; IPR00181; EGF_IRe.
InterPro; IPR001910; IG-IIRe.
InterPro; IPR001309; EGF_IRe.
InterPro; IPR001309; EGF_IRE.
InterPro; IPR001309; EGF_IRE.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000136; Sushi; SCR_CCP.
PRINTS; PR01365; ANTIFREEZEII.
                                                                                                                                                                                           MEDLINE=98094159; PubMed=9434070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF062402; AAC40166.1; -.
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SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
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PSAYQRTYSKYLKNSSSVKDNSINTSKHEHRWSRRWQETR
R -> RKWSFRKNGQPCFNKY (in isoform Vint).
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(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
                                                                                                                                                                                                                                                                       Glycoprotein, Proteoglycan, Lectin; Extracellular matrix, Sushi, Signal, Repeat; EGF-like domain, Calcium; Immunoglobulin domain, Byaluronic acid, Alternative splicing.
SIGNAL
21 2738 VERSICAN CORE PROTEIN.
NON CONS 348 349 1G-LIKE V-TYPE.
DOMĀIN 167 244 LINK 1.
DOMAIN 265 346 LINK 2.
DOMAIN 2349 695 GAG-ALPHA
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8.7%; Score 174; DB 1; Length 2738;
Best Local Similarity 28.5%; Pred. No. 5.1e-06;
Matches 47; Conservative 23; Mismatches 55; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING
C-TYPE LECTIN.
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2535 2539 AEREC -> NSARG (IN REF. 4).
2738 AA; 300004 MW; 12CA626D58BDBCGA CRC64;
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                         SMART; SM00409; IG; 1.

PROSITE; PR00010; LINK; 2.

PROSITE; PS00010; LASK HYDROXYL; 1.

PROSITE; PS00010; C_TYPE_LECTIN 1; 1.

PROSITE; PS00022; EGF 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01241; LINK; 2.
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SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
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Biol. Chem. 274:20444-20449(1999)
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                                           97 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
MEDLINE=9518135; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D., "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                           062059; Q62058; Q9CUU0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
STAIRA-STAIR-STBL/6, and Swiss Webster; TISSUE-Brain;
MEDLINE=9512251; PubMed=782336;
Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
Mulliphe forms of mouse PC-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.";
                                                                                                   153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 193
                                                                                                                                                                                                    PRT; 3358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1692 FROM N.A. (ISOFORM VI).
STRAIN=C57BL/6J; TISSUE=SKin;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues.";
J. Biol. Chem. 270:3914-3918(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM V3).
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                                                                                                                                                                                                    STANDARD;
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FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold-062059-4; Sequence=VSP 003087, VSP 003090;
TISSUB SPECIFICITY: V2 is found only in brain.
DEVELOPMENTAL STAGE: Disappears after the cartilage development.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 ink domains.
SIMILARITY: Contains 2 ESF-like domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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Signal, Repeat, EGF-like domain, Calcium, Immunoglobulin domain;
                                                                                                                                                                                                           SUBURIT: Inceracts with FBLNI.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
Event.Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
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PRINTS; PRO1265; LINKWODULE.
ProDom; PD000918; Link; 2.
ProDom; P000034; CCP; 1.
SWART; SW00034; CCP; 1.
SWART; SW00409; EGF_CA; 1.
SWART; SW00409; EGF_CA; 1.
SWART; SW00409; EGF_CA; 1.
SWART; SW004045; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; C_TYPE_LECTIN_2; 1.
PROSITE; PS01186; EGF_1; 2.
PROSITE; PS01186; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_1; 2.
PROSITE; PS01187; EGF_1; 2.
PROSITE; PS01187; EGF_1; 2.
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EMBL, D28599; -; NOT ANNOTATED CDS.
EMBL, AX014525; BAA06802.1; --
EMBL, AX014525; BAA06802.1; --
HSSP; P01132; 1EPG.
MGI:102889; CGPG.
INTERPO: IPR000152; Ask hydroxyl.
INTERPO: IPR001801; EGF Ca.
INTERPO: IPR001801; EGF Ca.
INTERPO: IPR001801; EGF Ca.
INTERPO: IPR001801; EGF Ca.
INTERPO: IPR001801; IGF CA.
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Pfam; PP00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                       hyaluronic acid.
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TISSUE=Placenta;
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                                                      RESULT 10
PGCV HUMAN
ID PGCV HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 96
                                                                                                                     EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
                                                                               GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F -> R (in isoform V1 and isoform V3)
/FTGAUSP 003087.
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1674 1680 TVWNSNS -> QFGIQTA (IN REF. 3).
3358 AA; 366938 MW; 071B80026BC0762D CRC64;
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/FTId=VSP_003088.
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                         PERSICAN CORE PROTEIN
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MISSING (IN REF. 3).
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; Pred. No. 6.8e-06;
23; Mismatches 55;
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TISSUE=Brain;
MEDLINE=95181355; PubMed=7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krusius T., Gehlsen K.R., Ruoslahti E.;
"A fibroblast chondroitin sulfate protesglycan core protein contains
lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90059882; PubMed=2583089;
Zimmermann D.R., Rucalahti B.;
"Multiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Naso M.F., Zimmermann D.R., Tozzó R.V.; "Characterization of the complete genomic structure of the human versican gene and functional analysis of its promoter."; J. Biol. Chem. 269:32999-33008(1994).
P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5; O1-JAN-1990 (Rel. 13, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 42, Last annotation update) Versican core protein precursor (Large fibroblast proteoglycan) Waluronate-binding protein) (GhAP).
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Dours-Zimmermann M.T., Zimmermann D.R.;
M. novel glycosaaninoglycan attachment domain identified in two alternative splice variants of human versican.";
J. Biol. Chem. 269:32992-32998(1994).
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MEDLINE=99327053; PubMed=10397680;
Lemire J.M., Braun K.R., Maurel P., Kaplan B.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wight T.N.; "Versican/PG-M isoforms in vascular smooth muscle cells.";
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MEDLINE-93122792; PubMed=1478664;
IOZZO R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM VO).
MEDLINE=95105188; PubMed=7528742;
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MEDLINE=88007514; PubMed=2820964;
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TISSUE=Glial tumor;
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                                                                                                            Incorporate Pi3611-5; Sequence-VSP 003086;

-1-TISSUE SPECIFICITY: Cerebral white matter. VO and VI is expressed in normal brain, gliomas, medulloblastomas, schwannomas, neurofibromas, and menningiomas; v2 is restricted to normal brain and gliomas; v3 is found in all these tissues except medulloblastomas.

-1- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 2 link domains.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 Subhi (SCR) domain.
-1- SIMILARITY: Contains 1 Subhi (SCR) domain.
-1- SIMILARITY: DELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                               -1- SUBUXT: Interacts with FBLN1 (By similarity).
-1- SUBUXT: Interacts with FBLN1 (By similarity).
-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-1- ALTERNATIVE PRODUCTS:
Evente-Alternative splicing; Named isoforms=5;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 118661; -.
GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005540; F:chondroitin sulfate proteoglycan; TAS.
GO; GO:0005540; F:hyaluronic acid binding activity; TAS.
GO; GO:0008037; P:cell recognition; TAS.
GO; GO:000775; P:development; TAS.
InterPro; IPR000152; Asx hydroxyl.
                                                                                                                                                                                                                                                                                     IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
                                                                                                                                                                                                                                                                                                                          IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
Arterjoscler. Thromb. Vasc. Biol. 19:1630-1639(1999)
                                                                                                                                                                                                                                                                                                      IsoId=P13611-3; Sequence=VSP_003084;
                                                                                                                                                                                                                                                                IsoId=P13611-1; Sequence=Displayed;
                             TISSUE=Brain;
BELINRE=89174663; PubMed=2466833;
Perides D. Lane W.S., Andrews D., Dahl
"Isolation and partial characterization
                                                                                Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U16306; AAA65018.1; EMBL; X15998; CAA34128.1; EMBL; X15998; AAB24878.1; EMBL; U2655; AAA67565.1; EMBL; D32039; BAA06801.1; EMBL; AP08145; AAA36437.1; EMBL; AF084545; AAA46845.1; PIR; S06014; A60979; PIR; S06014; A60979;
                                                                                         [9]
TISSUE SPECIFICITY OF ISOFORMS
                                                                      hyaluronate-binding protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:2464; CSPG2.
                     PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                    Name=V3;
                                                                                                                                                                                                                                                      Name=V0
                                                                                                                                                                                                                                                                          Name=V1
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97 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEGKLIEKFIENLLPSDGDF- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE.
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PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF 1; 2.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF 2; 1.

PROSITE; PS01187; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAG-BETA
                                                                    InterPro; IPR003006; Ig. MHC.
InterPro; IPR001306; Ig. MHC.
InterPro; IPR001308; Link.
InterPro; IPR000138; Link.
InterPro; IPR000138; Link.
InterPro; IPR000138; Link.
InterPro; IPR000138; Link.
IPR001099; Ictin_c; I.
IPR001099; Islink; 2.
IPRNT; SM0010918; Link; 2.
IPRNT; SM0010918; Link; 2.
IPRNT; SM0010918; Link; 2.
IPRNT; SM0010918; Link; 2.
IPRNT; SM00109; IGECT; I.
IPRNT; SM00109; IGECT; I.
IPRNT; SM00109; IGECT; I.
IPRNT; SM00109; IG; I.
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Ig_MHC.
Lectin_C.
EGF_Ca.
EGF_like.
Ig-Tike.
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MEDLINE=20507883; PubMed=10934210;

MEDLINE=20507883; PubMed=10934210;

MEDLINE=20507883; PubMed=10934210;

Medlecular and cellular properties of the rat A44 antigen, a C-type lectin-like receptor with structural homology to thrombomodulin.";

J. Biol. Chem. 275:34382-34392(2000).

-I- FUNCTION: Receptor (or element of a larger receptor complex) for Clq, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: Widely expressed in lung and heart. Expressed at lower level in brain, thymus, liver, spleen, intestine, kidney, adrenal gland, muscle and testis. Expressed on circulating natural killer cells.

-I- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                          ט
                                                                                                                                                                                                                                                                                                                                          STRAIN=PVG; TISSUE=Natural killer cells; MEDLINE=20545218; PubMed=11093152; LOVIK G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.; "Characterization and molecular cloning of rat ClqRp, a receptor on NK
                                                                                                                          Q9ETG1: Q9JIZ6;
28-FEB-2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement component Clg receptor precursor (Complement component Listophoromoonent, receptor 1) (ClgRp) (ClgR(p)) (Clg/MBL/SPA receptor)
(CD93 antigen) (Cell surface antigen AA4).
                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                     ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 331:0
153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; ISS. GO; GO:0004872; F:receptor activity; ISS. GO; GO:0016317; P:cell-cell adhesion; ISS. GO; GO:00042116; P:macrophage activation; ISS. GO; GO:0006909; P:phagocytosis; ISS.
                                                                                                          643 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           cella.";
Eur. J. Immunol. 30:3355-3362(2000)
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InterPro; IPR001881; BGF_Ca.
InterPro; IPR001809; BGF_Iike.
InterPro; IPR001304; Lectin_C.
Pfam; PF00008; BGF; S.
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF136537; AAG01572.1; -. EMBL; AF160978; AAF80402.1; -.
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                       09JIZ6;
                               3275
                                                                                                          CD93 RAT
                                                                                           CD93_RAT
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68 GQLVSIESEDEQXLIEKFIENLL---PSD---GDFWIGLRRREEKQSNSTACQDLYAWT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 GGGEDTTYSNWYKASKSSCISKRCVSLILDLSLKPHPSHLP-----KWHESPCGTP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LLLLGL---LGQLWAGAAADSEAVVCEG---TACYTAHW----GKLSAAEAQHRCNENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 VLLVGLRAATGRLLSGQP-----VCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDG
                                                                                                                                                                                                                                                        EGF-LIKE 1
EGF-LIKE 2
EGF-LIKE 3
EGF-LIKE 4, CALCIUM-BINDING (POTENTI)
EGF-LIKE 5, CALCIUM-BINDING (FOTENTIAL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                        COMPLEMENT COMPONENT C10 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGCV_CHICK STANDARD; PRT; 3562 AA.
090953; Q90945;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 8.6%; Score 172.5; DB 1; Length 643; Local Similarity 25.9%; Pred. No. 9.8e-07; Pred. S6; Conservative 37; Mismatches 74; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Indels
SMART; SM00034; CLECI, -..

SMART; SM00179; EGF CA; 3.

PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

PROSITE; PS0186; EGF 2; 3.

PROSITE; PS01187; EGF 2; 3.

PROSITE; PS01187; EGF 2; 3.

Cell adhesion; Receptor; Repeat; Signal; Transmembrane; EGF-like domain; Lectin; Glycoprotein.

23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> K (IN REF. 2).
9AE4C933AD943DB6 CRC64;
                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
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322
498
417
643 AA;
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TRANSMEM
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CARBOHYD
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3390 WIGL-----NDKMFERDFRWTDGSPLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 3439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 QRPCYKVIYFHDTSRRLNFBEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING (POTENTIAL).
                                                                         Glycoprotein, Proteoglycan, Lectin, Extracellular matrix, Sushi, Signal, Repeat, EGF-like domain, Calcium, Immunoglobulin domain, Hyaluronic acid, Alternative splicing.

1 POTENTIAL.

1 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.6%; Score 171; DB 1; Length 3562;
Best Local Similarity 28.5%; Pred. No. 1.3e-05;
Matches 47; Conservative 23; Mismatches 55; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9BC566E88C1602D2 CRC64;
                                                                                                                                                         PŌTENTIĀL.
VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE.
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EGF CA; 1.
IG LIKE; 1.
                           , PS50835; IG LIKE
; PS01241; LINK; 2
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                                                                                            SEQUENCE FROM N.A. (ISOFORMS VO AND V1).

STRAIN=White legiorn; TISSUB-Limb bud;

STRAIN=White legiorn; TISSUB-Limb bud;

A MEDLINE-93300846; PubMed-8314802;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida V., Ito K., Kimata K.;

Shinomura T., Nishida V., Ito K., Kimata K.;

Shinomura T., Nishida V., Ito K., Kimata K.;

spinced multiforms of PG-M, a large chondroitin sulfate proteoglycan

represed during chondrogenesis in chick limb buds. Alternative

T. Spilced multiforms of PG-M, and their relationships to versican.";

J. Biol. Chem. 268:14461-14469(1993).

J. Biol. Chem. 268:14461-14469(1993).

- I- FUNCTION: May play a role in intercellular matrix. May take part in

connecting cells with the extracellular matrix. May take part in

hyaluronic acid.

- HALTERMATIVE ROCATION: Secreted; extracellular matrix.

- ALTERMATIVE RODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
--- SIMILARITY: Contains 1 link domains.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lsoId=Q90953-2; Sequence=VSP 003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q90953-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWART; SW00022; CCF; 1.
SWART; SW00044; CLBCT; 1.
SWART; SW00049; IGF CA; 1.
SWART; SW00409; IGF 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00010; C_TYPE_LECTIN_1; 1.
PROSITE; PS00012; C_TYPE_LECTIN_1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0016152; EGF 2.
InterPro; IPR001611; EGF 2.
InterPro; IPR0016219; EGF 1ike.
InterPro; IPR001509; IG-like.
InterPro; IPR003109; IG-like.
InterPro; IPR0031006; IG-MHC.
InterPro; IPR001304; LG-MHC.
InterPro; IPR0001304; LG-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Link.
; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60226; CAA42787.1; -. EMBL; D13542; BAA02742.1; -.
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ProDom; PD000918; Link; 2.
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A47171; A47171.
HSSP; P00740; 1EDM.
                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=V0;
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POTENTIAL).
(POTENTIAL).

40; Gaps

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PGCA_BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; 028159;
01-JNN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antonsson P., Heinegaard D., Oldberg A., "The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.", J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 206:73-77(1986).

-1- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.

-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
MEDLINE=87270630; PubMed=3111460;
Oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perin J.-P., Bonnet F., Jolles J., Jolles P.;
"Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligonucleotide probe.";
PEBS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Cartilage;
MEDLINE-93352525; PubMed-8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perin J.P., Bonnet F., Jolles P.; "Structural relationship between link proteins and proteoglycan
3440 ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 3475
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
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IsoId=P13608-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 563-1056 FROM N.A.
MEDLINE=89380219; PubMed=2528543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arranged in homologous repeats."; Biochem. J. 243:255-259(1987).
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MEDLINE=85027710; PubMed=6489519;
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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ISOId=P13608-2; Sequence=VSP 003072;

DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION,
MAKES UP THE C-TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
AND G3.
                                                                                                                                                                                                    -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED (ABOUT 40) OLIGOSACCHARIDES.
-!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN ADULT AND FETAL BOVINE PROTSOGLYCANS.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
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R SWART; SM00034; CLECT; 1.

R SWART; SM00179; EGF CA; 1.

SMART; SM00179; EGF CA; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00010; CTYPE_LECTIN 1; 1.

R PROSITE; PS00129; EGF 1; 1.

R PROSITE; PS00130; EGF CA; 1.

R PROSITE; PS00130; EGF C
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LINK 2.
LINK 3.
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Asx_hydroxyl.
EGF_2.
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EMBL; L07053; -; NOT_ANNOTATED_CDS
PIR; 34234; A39808.
PIR; T42630; T42630.
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InterPro; IPR000152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2251 VVMIWHEKG------EWNDVPCNYQLPFTCKKGTVACGEPPVVEHARIFGQKKD 2298
                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                            CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P16112; Q13650;
01-ARR-1990 (Rel. 14, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
                                                                                                                                                                                                                                                                                                                                                 30 QPVCRGG---TQRPCYKVIYPHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
LINK 4.
23 X 6 AA APPROXIMATE TANDEM REPEATS OF
E-[EK]-P-F-P-S.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Chondrocytes;
MEDLINE=31093289; PubMed=1985970;
MEDLINE=31093289; PubMed=1985970;
Doege K.J., Sasaki M., Kimura T., Yamada Y.;
"Complete coding sequence and deduced primary structure of the human cartilage large aggregating proteoglycan, aggrecan. Human-specific repeats, and additional alternatively spliced forms.";
J. Biol. Chem. 266:894-902(1991).
                                     EGF-LIKE, CALCIUM-BINDING (POTENTIAL)
G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                     C-TYPE LECTIN.
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                                                                                                                                                                                                                                                                                                           7.9%; Score 158.5;
                                                                                                                                                                                                                                                                                FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 3).
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es 48; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=P16112-3; Sequence=VSP 003074, VSP 003075;
DOMAIN: TWO GLOBULAR DOMAINS. GI AND G2, COMPRISE THE AMINO DOMAIN: TWO CLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. GI CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LE BETWEEN G2 AND G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALTIX BIO1. 14:323-328(1994).

-I-FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTLIAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTLIAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.

-I-SUBUNIT: Interacts with FBLN1 (By similarity).
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SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 C-type lectin family similarity: SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTECCLYCAN FAMILY.
                                                                                                                                                                                    SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).
MEDILINE-89380154; PubMed=2789216;
MEDILINE-89380154; PubMed=2789216;
"A new epidermal growth factor-like domain in the human core protein for the large cartilage-specific proteoglycan. Evidence for alternative splicing of the domain.";
"J. Biol. Chem. 264:15747-15750(1989)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain of mammalian aggrecan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                   databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing, Named isoforms=3,
Comment=Additional isoforms seem to exist;
                                                                              Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ
OF 1778-2415 FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P16112-2; Sequence=VSP_003074;
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InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF
InterPro; IPR001110; Ig-like.
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MIM; 155760; -.
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HSSP; P98066; 1TSG.
                                     SSUE=Chondrocytes
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87 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 142
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2302 VVMIWHEKG------EWNDVPCNYHLPFTCKKGTVACGEPPVVEHARTFÖCKKD 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 29.1%; Pred. No. 8 9e-05;
Matches 52; Conservative 22; Mismatches 62; Indels 43; Gaps
657 657 N-LINKED (GLCNAC. .) (POTENTIAL).
737 N-LINKED (GLCNAC. .) (POTENTIAL).
858 1898 1898 N-LINKED (GLCNAC. .) (POTENTIAL).
163 2200 Missing (in isoform 2 and isoform 3).
7FTId=VSP 003074.
330 2390 Missing (in isoform 3).
7FTId=VSP 003075.
766 E -> A (IN REP. 4).
847 B -> A (IN REP. 4).
958 1928 E -> A (IN REP. 2).
959 1924 I -> V (IN REP. 2).
951 2391 A -> P (IN REP. 2 AND 3).
415 AA; 250191 MW; 1208937E1B98CGB6 CRC64;
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MEDLINE=97199258; PubMed=9047234;
Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;
notoming and primary structure analysis of ClqR(P), the human Clq/WBL/SPA receptor that mediates enhanced phagocytosis in vitro.";
Immunity 6:119-129(1997).
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MEDILINE=21640567; PubMed=11781389;
Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;
"Identification of human CD93 as the phagocytic Clq receptor (ClqRp)
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MEDLINE=21638749; PubMed=11780052;
Delouksa P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavridews G., Almeida J.P., Babbage A.K., Baguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Buller A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G.N., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSONPY3; 000274; Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
Complement component Clq receptor precursor (Complement component is eucomponent, receptor 1) (ClqRp) (ClqRp) (ClqRbL/SPA receptor)
(CD93 antigen) (CD93).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   7.9%; Score 158.5; DB 1; Length 2415; 9.1%; Pred. No. 8.9e-05;
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Leukoc. Biol. 71:133-140(2002).
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G2-B.
G2-B.
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12 X APPROXIMATE TANDEM REPEATS.
CS-1.
CS-2.
G3-B.
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Carefamon S., Hurt A.R., Hurt S.E., Osiviciti M.N.D. Gaillian J.L., Moden P. J., Huckle S. Holden J.L., Moden P. J., Huckle S. H., Hurt A.R., Hurt S.E., Osivoch N., Johnson C.M., Johns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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T -> V (IN REF. 1; AA SEQUENCE).

C -> T (IN REF. 1; AA SEQUENCE).

TA -> RI (IN REF. 1; AA SEQUENCE).

S -> N (IN REF. 1).

G -> A (IN REF. 1).

A A SEQUENCE.

S -> A (IN REF. 1; AA SEQUENCE).

R -> Q (IN REF. 1; AA SEQUENCE).
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                                                                                                                                                                                                                                          R MIM; 120577; -...

R GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0016037; P:cell-cell adheaion; IDA.
GO; GO:0016337; P:cell-cell adheaion; IDA.
GO; GO:0016391; P:cell-cell adheaion; IDA.
GO; GO:0016999; P:phagocytosis; NAS.
GO; GO:0016999; P:phagocytosis; NAS.
R InterPro; IPR001981; EGF_Ca.
R InterPro; IPR001981; EGF_Like.
R InterPro; IPR001304; Lecfin_C.
Pfam; PF00109; EGF, S.
R Pfam; PF01108; Tissue_fac; 1.
Ffam; PF01108; Tissue_fac; 1.
R SMART; SM00179; EGF_CA: 3.
R RSMART; SM00179; EGF_CA: 3.
R PROSITE; PS0010; ASX HYDROXYL; 3.
R PROSITE; PS01186; EGF_C3: 3.
R PROSITE; PS01186; EGF_C3: 3.
Cell adheaion; Receptor; Repeat; Signal; Transmembrane;
R EGFAIL CENTAL
R EGFAIL GOMAIN; EGF_CA: 3.
Cell adheaion; Receptor; Repeat; Signal; Transmembrane;
R EGFAIL
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EGF-LIKE 2.
EGF-LIKE 3, CALCIUM-BINDING (P
EGF-LIKE 5, CALCIUM-BINDING (P
EGF-LIK
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C-TYPE LECTIN.
                                                                                                                                                     EMBL; U94333; AAB53110.1; -.
EMBL; AL118508; CAC00597.1; -.
EMBL; BCO28075, AA428075.1; -.
HSSP; P35555; IEMN.
Genew; HGNC:15855; C1QR1.
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70 LVSIESEDEQKLIEKFIENLLPSD-----GDFWIGLRRREEKQSNSTACQDLYAWT-D 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.9%; Score 157.5; DB 1; Length 652; Best Local Similarity 25.2%; Pred. No. 1.8e-05; Matches 53; Conservative 40; Mismatches 84; Indels 33; Gaps
       504 504 R -> G (IN REF. 1; AA SEQUENCE).
541 541 P -> S (IN REF. 1).
652 AA, 68560 MW, EECAOFEAC55FCAC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 ---FICKYSDEKPAVPSREAEGEETELTTP 200
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 16:06:34 Run on:

; Search time 18.1827 Seconds (without alignments)
1978.090 Million cell updates/sec

Perfect score:

US-09-887-855-2 2000 1 MRPGTALQAVLLAVLLVGLR......PDQMGRSKESGWVENEIYGY 374 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		مبن			SUMMAKIES	
Result No.	Score	Query	Length	DB	TI.	Dood
				H		TOTOG TOTOG
1	183	9.5	1456	-	A36563	mannose receptor p
7	178.5		1455	-	A48925	
٣	177		26	~	S52781	
4	174.5	8.7	1643	7	T14274	ū
Ŋ	174.5	8.7	3381	~	T42389	
ø	174	8.7	1257	7	S28764	
7	174		2397	-	A55535	
80	174	8.7	2409	-	A60979	
6	171	9.8	3562	~	A47171	
10	170.5		1479	~	T42710	mannose receptor.
11	158.5	•	1340	~	A39808	proteoglycan core
12	158.5	•	2327	~	T42630	addrecan - bovine
13	158.5	7.9	2415	-	A39086	addrecan precursor
14	156	7.8	162	٦	LNRC1	lectin BRA3-1 pred
15	154.5	7.7	612	~	B42755	E-selectin precure
16	153.5	7.7	2124	N	A28452	proteoglycan core
17	152	7.6	912	~	A54423	brevican precursor
18	151		162	٦	LNRC3	lectin BRA3-2 prec
19	.50.5	7.5	459	7	T24425	hypothetical prote
20	150	7.5	330	~	T46256	brevican - human (
21	149	7.4	321	-	LINHUER	IGE FC receptor II
22	148.5	7.4		7	JC4690	
23	148.5	7.4		~	A46274	HIV gp120-binding
24	148.5	7.4	2132	Н	A55182	addrecan precureor
25	148	7.4	253	~	E89130	
56	147	7.3	883	~	857653	brevican precursor
27	146	7.3	2109	-	I50421	
28	145.5	7.3	742	7	JC7595	scavenger recentor
29	145	7.2	883	~	\sim	brevican precursor

lectin - barnacle	L-selectin precurs	coagulation factor	L-selectin precure	hypothetical prote	hypothetical prote	bitiscetin alpha c	phospholipase-A(2)	reg I, regeneratin	IgE Fc receptor, 1	L-selectin precurs	pulmonary surfacta	pulmonary surfacta	pulmonary surfacta	lectin precursor -	lectin - Iberian r
S10548	823936	JC4329	A32375	T26655	T26152	JC5058	S48719	A47148	LINMSER	S22124	LNHUPS	LNHUP6	LNHUP1	LNFHLS	S32489
~	~	~	-4	~	~	~	~	~	H	7	-	-	-	-	~
173	372	129	372	463	321	131	1487	165	331	370	248	248	248	283	172
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	7.2	7.2	7.2	7.2	7.1	7.1	7.3	7.1	7.1	7.0	7.0	7.0	7.0	7.0	6.9
7.2	144.5 7.2	•		•	•	•	•	•	•	•	•	•	•	•	138.5 6.9

ALIGNMENTS

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mannose receptor precursor - human
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Cispecies: Homo sapicates (man)
Cispecies: Homo sapicates (man)
Cispecies: Homo sapicates (man)
Cispecies: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
Ciccession: A36563; A60926; A44255; B44255; B44255; B44255; F44255; F44

.;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1313, 'T', 1335-1456 <EZE>
A;Cross-references: GB:X55635
A;Note: translation of the nucleotide sequence is incomplete
A;Note: translation of the nucleotide sequence is incomplete
A;Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497
B;Kim, S.J; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A;Title: Organization of the gene encoding the human macrophage mannose receptor (MRCI)
A;Reference number: A44255, MUID:93052405; PMID:1294118

A.Molecule type: DNA A;Residues: 155-233, KSAL', 238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865; A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428 A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A Map position: 10p13-10p13
C; Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II r
C; Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II r
C; Superfamily: phospholipase A2 receptor; transmembrane protein
C; Seywords: dipal sequence #status predicted <SIG>
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 168-209/Domain: fibronectin type II repeat homology <LCHI>
F; 223-340/Domain: C-type lectin homology <LCHI>
F; 362-486/Domain: C-type lectin homology <LCHI> C,Genetics: A,Gene: GDB:MRC1 A,Crose-references: GDB:133759; OMIM:153618

54; Query Match
9.2%; Score 183; DB 1; Length 1456;
Best Local Similarity 25.1%; Pred. No. 1.2e-06;
Matches 53; Conservative 38; Mismatches 66; Indels 54

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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiDate: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
CiAccession: 552781
RiRauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
RiRauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
A;Description: Amino acid sequence of mouse neurocan and brevican and their different exterence number: 552781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X84727; NID:9758629; PIDN:CAA59216.1; PID:9758630
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EK
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: BGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
F;1167-1123/Domain: Complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      versican precursor, splice form V2 - bovine
Cispecies: Bos primigenius taurus (cattle)
Cidate: 20-8p-1999 #sequence_revision 20-8ep-1999 #text_change 05-May-2000
CiAccession: T14274
Rischmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine bra.
A;Reference number: 217954; MUID:98288320; PMID:9624174
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A;Molecule type: mRNA
A;Residues: 1.1643 <SCH>
A;Cross_references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKPIENLLPSDGDFW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048 QGHCYR--YF---AHRRAWEDARRCRRRAGHLISVHSPREHKFINSF-----GHENSW
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C;Keywords: glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels
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8.7%; Score 174.5; DB 2;
Best Local Similarity 25.5%; Pred. No. 6.8e-06;
Matches 59; Conservative 26; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.8%; Score 177; DB 2;
Best Local Similarity 31.5%; Pred. No. 3.1e-06;
Matches 45; Conservative 17; Mismatches 49;
                                                                                       CFKIFGFANEEKKSWQDARQACKGL 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RWNDVPCNYNLPYVCK 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 IGGPYMFQWNDDRCNMKNNFICK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: brain
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A; Accession: T14274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S52781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                             209
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Gispecies; wis musculus (house mouse)

Gispecies; wis musculus (house mouse)

Giscession: A88325; 23120; PC2245

Ribarris, N.; Supper, M.; Rite, M.; Chang, G.; Ezekowitz, R.A.

Blood 80, 2352-2373; JUNID: 93041353; PMID: 412407

A;Reference number: A48925; MUID: 93041353; PMID: 412407

A;Reference number: Muit conceptual translation

A;Reference number: Muit conceptual translation

A;Reference number: Muit Rite, M.; Chang, G.; Ezekowitz, R.B.

A;Reference number: S21320

A;Reference number: PREMILIZITY, FE, 1119-1455 cHA2>

A;Reference number: S21320

A;Reference number: PREMILIZITY, FE, 1119-1455 cHA2>

A;Reference 
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---TMPSVPSGCKEGWNFYSN 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 ---WhDINCGYPNNFICORHNSINATAMP-----TTPTTPGGCKEGWHLYKNK 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY
                                                                                                                                                                                 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTWY----SNSGF----
                                                                                                                                                                                                                                                         160 MFOWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 MFQWNDDRCNMKNNFICK---YSDEKPAVPSREAEGEETELTTPVLPEETQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1455;
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25.9%; Pred. No. 2.7e-06;
tive 33; Mismatches 66
                                                                                                                                                                                                                                                                                                       KCFKIFGFMEEERKNWQEARKACIGFGGNLV 985
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Matches 53; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: ASSS35
R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generat
A;Reference number: ASSS35; MUID:95122551; PMID:7822336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2397 <RES>
A;Cross-references: GB:D16263; NID:g862460; PIDN:BAA03796.1; PID:g862461
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; F;1-20/Domain: signal sequence #status predicted <SIG>F;21.1654/Domain: signal sequence #status predicted <AMT>
F;21-1654/Domain: link protein repeat homology <LNKL>
F;255-346/Domain: link protein repeat homology <LNKL>
F;255-346/Domain: link protein repeat homology <LNKL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycar
P;1-22/Domain: signal sequence #status predicted <SIG>
P;23-1257/Product: neurocan #status predicted <MAT>
P;23-1257/Product: neurocan #status predicted <MAT>
P;276-253/Domain: link protein repeat homology <LNK1>
P;776-253/Domain: link protein repeat homology <LNK2>
P;364-366(Region: cell attachment (R-G-D) motif
P;364-366(Region: cell attachment (R-G-D) motif
P;353-984/Domain: GF+PD>
P;1029-1149/Domain: C-type lectin homology <LCH>
P;1029-1149/Domain: complement factor H repeat homology <FHD>
P;1156-1212/Domain: complement factor H repeat homology sell fattatus predicted
P;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
P;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2179 GGGCYK--YF---AHRRTWDAAERECRLOGAHLTSILSHEEOMFVNRV-----GHDYO 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 WIGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-'96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 ORPCYKVIYFHDTSRRLNFEBAKBACRRDGGQLVSIESEDBQKLIEKFIENLLPSDGDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
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F;2133-2164/Domain: EGF homology <EG2>
F;2171-2291/Domain: C-type lectin homology <LCH>
F;2278-2354/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
8.7%; Score 174; DB 2;
Best Local Similarity 30.8%; Pred. No. 5.4e-06;
Matches 44; Conservative 18; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N, Contains: glial hyaluronate-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 IGGPYMFQWNDDRCNMKNNFICK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 versican precursor - mouse
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Matches
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Variation precursor, splice form VO - bovine
NyAlternate names: chondroitin sulfate proteoglycan
Cispecies: Bos priniganius raurus (cattle)
Cispecies: Bos priniganius raurus (cattle)
Cispecies: Bos priniganius raurus (cattle)
Cispecies: Bos priniganius carrus (cattle)
Cispecies: Bos priniganius carrus (cattle)
Rischmalfeldt, Mr. Dourse Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15788-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine brain A;Reference number: Z17954; MUID:98288320; PMID:9624174
A;Reference number: Z17954; MUID:98288320; PMID:9624174
A;Residues: T42389
A;Residues: 17331 < SCH>
A;Residues: 17331 < SCH>
A;Cross-references: EMBL:AF060456; NID:93253299; PID:93253300; PIDN:AAC24358.1
C;Superfamily: chicken chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
C;Reywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F;1-20/Domain: signal sequence #status predicted <AMT>
F;21-3381/Product: versican, splice form VO #status predicted <AMT>
F;57,331,352,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2299,2356,26
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A;Molecule type: mRNA
A;Residues: 1-1257 <RANA
A;Residues: 1-1257 <RANA
A;Residues: 1-1257 <RANA
Cross-references: EMBL:M97161; NID:9205649; PIDN:AAC37679.1; PID:9205650
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; C;Keywords: chondroitin sulfate proteoglycan; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, A;Reference number: S28764; MUID:92406907; PMID:1326557
                                                                                                                                                                                                               11;
                           97 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 152
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3210 WIGL------NDKMFEHDFRWIDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF-
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                                                                                                                                                                                                                                                                                                                                               1573 KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3311 KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 3361
                                                                                                                                                                                                                                                                                                  ----ETELTT------PVL----PEETQEEDAKKTFKESREAALN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PVL----PEETQEEDAKKTFKESREAALN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 174.5; DB 2; Length 3381; 25.5%; Pred. No. 1.7e-05; tive 26; Mismatches 71; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-----
                                                                                                                                                                  153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 25.54 tes 59; Conservative
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Length 2409;

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F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>F;2106-2137/Domain: BGF homology <EG1>
F;2106-2137/Domain: BGF homology <EG2>
F;2144-2175/Domain: BGF homology <EG2>
F;2182-2302/Domain: C-type lectrin homology <LCH>
F;2180-2305/Domain: C-type lectrin homology <PHD>
                                                                                                                                                                                                                                                                                                                                                              Query Match
8.7%; Score 174; DB 1;
Best Local Similarity 28.5%; Pred. No. 1.2e-05;
Matches 47; Conservative 23; Mismatches 55.
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Best Local Similarity 28.54
Matches 47; Conservative
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Angessence manner: 353284

Angessence manner: 358440; 1094-1185;1191-2246 < VAO.

R. Bignamia: A.; Lates of W. S.; Andrews D. Dahl, D.

R. Bignamia: A.; Daved W. S.; Andrews D. Dahl, D.; Bignami, A.

Angession: A60979; WID: 8922989; PMID: 246524

Ancession: A60999; WID: 8922989; PMID: 246524

Ancession: A60999; MID: 8922989; PMID: 246524

Ancession: A3038; MID: 89245897

Angestiuse: 1712-210, 288-308

Angestiuse: A3038; MID: 89345897

Angestiuse: A30389; MID: 89345899

Angestiuse: A30389; MID: 89345997

Angestiuse: A30389; MID: 89345997

Angestiuse: A30389; MID: 89345997

Angestiuse: A30389; MID: 8934599

Angestiuse: A30389; MID: 9934599

Angestiuse: A30389; MID: 9934599

Angestiuse: A30389

Angest
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A, Readduds: 1-2409 (21XM)
A, Crose-references: GB:XINS
A, Crose-references: GB:XINS98; NID:937662; PIDN:CAA34128.1; PID:937663
R; Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A; Title: Identification of the proteoglycan versican in aorta and smooth muscle cells
A; Reference number: S43921; MUID:95005762; PMID:7921538
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C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
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A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Experimental source: stage 22-23 developing limb buds
A;Experimental source: stage 22-23 developing limb buds
A;Mole: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superfamily: chicken chondroin neglat homology cLNK1>
F;264-345/Domain: link protein repeat homology cLNK2>
F;258-3289/Domain: EGF homology cEGF1>
F;3258-3289/Domain: EGF homology cEGF1>
F;3296-3327/Domain: EGF1-
                                                                        2190 QGQCYK--YF---AHRRTWDAAERECKLQGAHLTSILSHEEQMFVNRV-----GHDYQ 2237
                                                                                                                                                                                                                                                                                                                                         2238 WIGL------NDKMPEHDFRWTDGSTLOYENWRPNOPDSPFSAGEDCVVIIWHENG-- 2287
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                                                                                                                                                                                                                                                   97 WIGLRRREEKQSNSTACQDLYAWTDGSISQPRNWYVDEP----SCGSEVCVVMYHQPSAP 152
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38 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3342 QGQCYK--YF---AHRRTWDTAERECRLQGAHLTSILSHEEQVFVNRI------GHDYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Indela
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F;3461-3517/Domain: complement factor H repeat homology <PHD>
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28.5%; Pred. No. 3.5e-05;
tive 23; Mismatches 55
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Gispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: 11-3an-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
Cipate: 11-3an-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
Cipate: 11-3an-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
Ridcession: T42630
Aibescription: Complete coding sequence of bovine aggrecan: comparative structural ana Aibescription: Complete coding sequence of bovine aggrecan: comparative structural ana Aibescription: Complete coding sequence of bovine aggrecan: comparative structural ana Aibescription: Complete coding sequence of bovine aggrecan: comparative structural ana Aibescription: Cattles
Aibescription: Complete coding sequence of bovine aggrecan: Cattles
Aibescription: Complete coding sequence of bovine aggrecan: Cattles
Aibescription: Complete coding sequence of bovine aggrecan: Cattles
Aibescription: Complete coding sequence cattles
Cisuperfamily: aggrecan: C-type lectin homology; complement factor H repeat homology; likeywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycopr
                                   A.A.Ccession: E29164
A.Molecule type: protein
A.R.Ccession: E29164
A.Molecule type: protein
A.Residues: 1230-1249 < PE2.
C.Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;
C.Superfamily: aggrecan; C-type lectin homology (fragment) <LNKI>
F.92-56/Domain: link protein repeat homology (fragment) <LNKI>
F.92-56/Domain: link protein repeat homology (fragment) <LNKI>
F.90-146/Domain: link protein repeat homology (fragment) <LNKI>
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F.1130-1256/Domain: C-type lectin homology <LKI+>
F.1130-1256/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggrecan precursor, cartilage long splice form [validated] - human NyAlternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; N;Contains: aggrecan cartilage short splice form C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 VVMIWHEKG------EWNDVPCNYQLPFICKKGTVACGEPPVVEHARIFGQKKD 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQPRNWYVDEP----SCGSEV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 QPVCRGG---TQRPCYKVIYFHDTSRRLNFBEAKBACRRDGGQLVSIESEDEQKLIEKFI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 CVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVVMYHQPSAPAGIGGPYMPQWNDDRCNMKNNPICKYS----DEKPAVPSREAEGEETE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2165 NN---NAQDYQWIGL-----NDKTIEGDFRWSDGHSLQPENWRPNQPDNFPATGEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.9%; Score 158.5; DB 2; Length 2
26.8%; Pred. No. 0.00022;
tive 29; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
              A; Reference number: A91327; MUID:85027710; PMID:6489519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 7.9%; Score 158.5; DB 2
Local Similarity 26.8%; Pred. No. 0.00011;
hes 48; Conservative 29; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.8%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggrecan - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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A;Wolecule type: mRNA
A;Residues: 622-1340 
CLD>
A;Residues: 622-1340 
CLD>
A;Residues: 622-1340 
CLD>
A;Reference number: A39808; MUID:91217051; PMID:2022637
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of A;Reference number: A39808; MUID:91217051; PMID:2022637
A;Reference number: Drotein
A;Residues: 1-28;59-82;131-137, QSET, 142-149;196-207;226-249;1137-1143;1252-1267;1274-1
B;Perin, J. P.; Bonnet, F.; Jolles, P.
R;Perin, J. P.; Bonnet, F.; Jolles, P.
R;Residues: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A27751
A;Molecule type: protein
A;Feducis: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
B;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomed
                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          profeoglycan core protein, cartilage - bovine (fragments)
Nylternate names: aggregating cartilage proteoglycan
Nylternate names: aggregating cartilage proteoglycan
Nylternate names: aggregating cartilage proteoglycan
C;Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C;Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
Nylten 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
Nylten 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
Nylten 264, 16170-16173, 1989
Nylten 17he keartan sulfate-enriched region of bovine cartilage proteoglycan consists of A;Reference number: A34234; MUID:89380219; PMID:2528543
                         R.W. K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
J. Biol. Chem. 271, 21323-21330, 1996
J. Biol. Chem. 271, 21323-21330, 1996
A.Fitle: Characterization of a novel member of the macrophage mannose receptor type C JARCESSION: T42710
A.Accession: T42710
A.Accession: T42710
A.Accession: T42710
A.Accession: T42710
A.Molecule type: mRNA
A.Residues: 1-1479 «WUX>
A.Residues: 1-1479 «WUX>
C.Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II D.C. Keywords: membrane protein; receptor
C.Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>
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R)Coldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259.
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from
A;Reference number: A27752; MUID:87270630; PMID:3111460
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; Score 170.5; DB 2; 11.4%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; Preco. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Conservative
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A;Residues: 128-621 <ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
Accession: T42710
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Query Match 7.9%
Best Local Similarity 29.1%
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
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A, Residues: 'V', 404-405, 'XX' < FOS>
R, Wolecule type: protein
A, Residues: 'V', 404-405, 'XX' < FOS>
R, Wolecule type: protein
A, Residues: 'V', 404-405, 'XX' < FOS>
R, Wolecule type: Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
B, Biochem, J. 313, 933-940, 1996
A, Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A, Recession: S62786; MUD: 96190740; PMID: 8611178
A, Accession: S62786; MUD: 96190740; PMID: 8611178
A, Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 < DUD>
A, Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 < DUD>
A, Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 < DUD>
A, Residues: 1778-1927, 'A', 1929-1963, 'V', 1965-2162, 2201-2415 < DuD>
A, Residues: 178-1927, 'A', 1929-1963, 'V', 1965-2069, 'A', 2071-2415 < BAD>
A, Residues: 1936-1963, 'V', 1965-2069, 'A', 2071-2415 < BAD>
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A, Residues: 1936-1963, 'V', 1965-2069, 'A', 2071-2415 < BAD>
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A, Residues: 1936-1963, 'V', 1965-2069, 'A', 2071-2415 < BAD>
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A, Residues: 1936-1963, 'A', 1965-2069, 'A', 2071-2415 < BAD>
A, Residues: 1936-1963, 'A', 1965-2069, 'A', 20
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A;Reidues: 361-370, X',372-373;393-399,'X',401-407,'X',409 <SAN>
A;Residues: 361-370, XN',372-373;393-399,'X',401-407,'X',409 <SAN>
A;Cross-references: PIDN:AAB22079-1; PID:g248844; PIDN:AAB22077.1; PID:g248842; PIDN:AABA;Experimental source: synovial fluid
A;Experimental source: synovial fluid
A;Note: sequences modified after extraction from NCBI backbone
           C43
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A; Residues: 764-765, A; 767-846, V', 848-862, X', 864 <BAR>
A; Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A; Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A; Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue 8; NID:g807128
A; NID: M.Z.; Mox, M.Z.; Hughes, C.E.; Handley, C.J.
Arch. Biochem. Biophys. 322, 22-30, 1995
A; Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the A; Reference number: S66389
A; Reference number: S66389
A; Residues: II-23; 44, X', 26-27; 393-401; 402-403 <III.>
A; Residues: II-23; 44, X', Z6-27; 393-401; 402-403 <III.>
A; Residues: II-23; 44, X', Z6-27; 393-401; 402-403 <III.>
A; Risbande. Secondary A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
A; Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A; Reference number: S6646; MUID:96181659; PMID:8603731
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A;Residues: 350-497 <GLU5
A;Cross-references: EMBL:X80278; NID:g516295
A;Cross-references: EMBL:X80278; NID:g516295
A;Note: this translation is not annotated in GenBank entry HSAGGREC, release 113.0
B;Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
J. Clin. Invest. 89, 1512-1516, 1992
A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
                                        R, Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
J. Biol. Chem. 266, 894-902, 1991
A, Title: Complete coding sequence and deduced primary structure of the human cartilage
A, Reference number: A39086; MUID:91093289; PMID:1985970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissues
С;Acceвsion: A39086; S50206; A43919; S46559; S66389; S68646; S62786; A34226; B43919;
R;Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Residues: 1-2162, 2201-2329, 'A', 2392-2415 <DOE>
A; Cross-references: GB:M55172; NID:g178258; PIDN:AAA62824.1; PID:g178259
R; Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A; Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal A; Reference number: S50206; MUID:95035091; PMID:7524681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A43919; MUID:92235266; PMID:1569188
A;Accession: A43919
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A;Cross-references: GB:J05062; NID:g181167; PIDN:AA35726.1; PID:g181168
C;Genetics:
A;Gene: GB:AGC1; CSPG1; CSPGCP; MSK16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamally: aggreean, C-type lectin homology; complement factor H repeat homology; E
C;Superfamally: aggreean, C-type lectin homology; complement factor H repeat homology; E
C;Sevords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracel
F;10-2162,2201-2415/Product: aggreean cartilage short splice form #status predicted
F;20-2162,2201-2415/Product: aggreean cartilage short splice form #status predicted
F;20-2162,2201-245/Product: aggreean short splice form #status predicted
F;20-2162,2201-245/Product: aggreean short splice form #status predicted
F;20-2162,2201-245/Product: aggreean homology <LNK1>
F;20-2162,2201-245/Pomain: link protein repeat homology <LNK2>
F;268-349/Domain: link protein repeat homology <LNK2>
F;268-349/Domain: link protein repeat homology <LNK3>
F;20-2162/Domain: link protein repeat homology <LNK3>
F;21-2162/Domain: link protein repeat homology <LNK3>
F;21-2162/Domain: link protein repeat homology <LNK3>
F;21-2152/Domain: link protein repeat homology <LNK3>
F;21-2152/Domain: chondroitin sulfate attachment #status predicted <KS3>
F;210-2152/Domain: chondroitin sulfate attachment #status predicted <CS1>
F;210-21539/Domain: Complement factor H repeat homology <FHD>
F;2132-238/Domain: C-type lectin homology <LNK3>
F;2132-238/Domain: C-type lectin homology <LNK3>
F;2132-238/Domain: C-type lectin homology <LNK3>
F;2135/Domain: Complement factor H repeat homology <FHD>
F;2135/Domain: C-type lectin homology <LNK3>
F;2136/Domain: C-type lectin homology <LNK3>
F;2137,314,314,602,657,717,11898/Binding site: carbohydrate (Asn) (covalent) R;317,376/Binding site: Rera
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A;Molecule type: protein
A;Residues: 25-145, K',147-162 <MUR>
A;Rote: 146-Arg was also found
C;Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development C;Comment: The molecule is a tetramer of identical chains.
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R; Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A; Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa. A; Reference number: A26094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2302 VVMIWHEKG------EWNDVPCNYHLPFTCKKGTVACGEPPVVEHARTFGOKKD 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.; Kamiya, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Megabalanus rosa
C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JC1503; A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2202 QEVCEEGWNKYQGHCYR--HFPD---RETWVDAERRCREQOSHLSSIVTPEEQ----EFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2253 NN---NAQDYQWIGL-----NDRTIEGDFRWSDGHPMQFENWRPNQPDNFFAAGEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPVCRGG---TQRPCYKVIYFHDTSRRLNPEEAKEACRRDGGQLVSIESEDEQKLIEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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A; Introns: 22/1; 47/2; 86/3
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: hemolymph; homotetramer; lectin
F;1.24/Domain: aignal sequence #status predicted <SIG>F;25-162/Product: lectin BRA3-1 #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.9%; Score 158.5; DB 1
29.1%; Pred. No. 0.00023;
tive 22; Mismatches 62
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Search completed: December 22, 2003, 16:14:40
Job time : 20.1827 seca
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A; Residues: MRATAGV', 1-389, 391-612 < wr.
A; Residues: MRATAGV', 1-389, 391-612 < wr.
A; Residues: MRATAGV', 1-389, 391-612 < wr.
A; Residues: MRATAGV', 1-389, 391-612 

    A; Residues: MRATAGV', 1-389, 391-612 
    MD10 : Sequences: General cells

    A; Note: the sequence in General WOSERLEC, release 117.0, (FIDN:AAA37577.1; PID:gl
A; Note: ti se uncertain whether the initiator is Met. 1 or the AUG codon preceding that
C; Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology;
C; Reywords: glycoprotein; renamembrane protein
F; 1-21/Domain: signal sequence #status predicted < SIG>
F; 1-21/Domain: C-type lectin homology < LCH>
F; 1-21/Domain: Complement factor H repeat homology < FH1>
F; 143-114/Domain: complement factor H repeat homology < FH2>
F; 305-363/Domain: complement factor H repeat homology < FH3>
F; 308-426/Domain: complement factor H repeat homology < FH3>
F; 308-426/Domain: complement factor H repeat homology < FH3>

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;Species: Mus musculus (house mouse)
;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
;Accession: S23174; B42755
;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
ur. J. Biochem. 206, 401-411, 1992
;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and func
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Residues: 1-612 <BEC>
A)Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
A)Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
B;Weld: A: Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, I5176-15183, 1992
A)Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectins, Reference number: A42755; MUID:92340571; PMID:1378846
                                                                                                                                                                                                                                                                                                                                                                                                                                   EACR--RDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 WTDGSISQFRNWYVDEPS-----CGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKN 172
                                                                                                                                                                                                                                                                                                   1 MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFBBAK 60
                                                                                                                                                                                                                                                                                                                                                   25,391,528/Binding Site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                      Query Match 7.8%; Score 156; DB 1; Length 162; Best Local Similarity 24.9%; Pred. No. 1.3e-05; Matches 46; Conservative 30; Mismatches 67; Indels
F;26-150/Domain: C-type lectin homology <LCH>
F;26-39,56-150,125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental
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27.9%; Pred. No. 9e-05;
tive 28; Mismatches 45;
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Best Local Similarity 27.9
Matches 38; Conservative
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Gaps

Indels

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106 KQSNSTACQDLYAWTDGS---ISQFRNWYVDEPS--CGSEVCVVWYHQPSAPAGIGGPYM 160
                                                                                                                                                     46 YFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREE 105
                                    23 YYNASSELMTYDEASAYCQRDYTHLVAIQNKEE---INYLNSNLKHSPSYYWIGIRK---
                                                                                                                                                                                                                                     161 FOWNDDRCNMKNNFIC 176
                                                                                                                                                                                                                                                                       125 --WNDERCNKKKLALC 138
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EACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWT 120
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Pacent No. US20020058310A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Anderson, Dirk M
TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
FILE REFERENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
US-09-904-859-137
US-09-904-137
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US-09-904-137
US-09-906-646-137
US-09-906-700-137
US-09-906-100-137
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    ORGANISM: Homo sapiens
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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APPLICANT: BAUGHN, Mariah R.
APPLICANT: BUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: AL, VOUNG, Janice
APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REPERBNCE: PP.0760 PCT
CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT PILING DATE: 2002-06-10
FRIOR PAPLICATION NUMBER: 60/172,852; 60/172,354
FRIOR PAPLICATION NUMBER: 60/172,852; 60/172,354
SPIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE PERL PROGram
SEQ ID NO 15
LENGTH: 374
                                                                                                                         VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRP
                          241 VITVVCWVWICKKRREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRP
                                                                                              DLKNISPRVCSGRATPDDMSCDYDNMAVNPSESGPVTLVSVESGPVTNDIYEPSPDQMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1
US-10-149-819-15
                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15, Application US/10149819; Publication No. US20030044913A1; GENERAL INFORMATION:
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APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. TOM
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Best Local Similarity 100.0
Matches 374; Conservative
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ORGANISM: Homo sapiens
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                                                  241 VITVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRP
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                       VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRP
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 2000, Application US/10094749

| Publication No. US2003019741A1
| GENERAL INFORMATION:
| APPLICANT: SUGITAMA, TOMOXASU
| APPLICANT: SUGITAMA, TOMOXASU
| APPLICANT: WARMATON, AI
| APPLICANT: WARMATON, AI
| APPLICANT: SHII, SHIZUKO
| APPLICANT: YOUND APPLICANT: YOUND APPLICANT: YOUND APPLICANT: YOUND APPLICANT: THIE, RYOTARO
| APPLICANT: TAMAOTO, JUN-ICHI
| APPLICANT: YOUND APPLICANT: TOSUKA, KAORU
| APPLICANT: TOSUKA, KAORU
| APPLICANT: TOSUKA, KAORU
| APPLICANT: TOSUKA, KAORU
| APPLICANT: TOSUKA, MOTOVUKI
| APPLICANT: TOSUKA, MOTOVUKI
| APPLICANT: MAGHIKO
| APPLICANT: WAGHIKO
| APP
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; ORGANISM: Homo sapiens
US-10-094-749-2090
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APPLICANT: Tumes, Denies, A.

APPLICANT: Williams, P. Mickey
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANTON: Acids Encoding the Same
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14.

FILE REPERENCE: 10466-14.

FILE REPLICATION NUMBER: US/09/09.320
CURRENT FILING DATE: 2000-02-22
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR PLICATION NUMBER: US/0146,202
FRIOR PLICATION NUMBER: US/0146,203
FRIOR PLICATION NUMBER: PCT/US99/2094
FRIOR PLICATION NUMBER: PCT/US99/2094
FRIOR PLICATION NUMBER: PCT/US99/2094
FRIOR FILING DATE: 1999-09-15
FRIOR PLICATION NUMBER: PCT/US99/2094
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                              Sequence 137, Application US/09909320
GENERAL IN-US/20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bostsein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
                                 361 SKESGWVENEIYGY 374
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Gerritsen, Mary E
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361 SKESGWVENEIYGY 374
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: OTSUKA, KAORU
APPLICANT: IRIE, KYOTAKO
APPLICANT: TRAECHIKA, ICHIRO
APPLICANT: SEKI, NAGHIKO
APPLICANT: SOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: MAGHIKI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR SEQ ID NOS: 3381
                                                                                                                                                                                                                   Sequence 2142, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKANATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
                     361 SKESGWVENEIYGY 374
                                                      361 SKESGWVENEIYGY 374
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; ORGANISM: Homo sapiens
US-10-094-749-2142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 IPLILLLVVTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSE 292
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                CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
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PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-16
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PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
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PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2099-13-30
PRIOR PILING DATE: 20
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                    1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR
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                                                                                                                                                                                                                Length 382;
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Best Local Similarity 97.9%; Pred. No. 2.7e-178;
Matches 374; Conservative 0; Mismatches 0;
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Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botesin, David
APPLICANT: Betesin, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Tumas, Daniel
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Paoni, Nicholas F.
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Gerritsen, Mary E.
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
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                                                                                                                          ; ORGANISM: Homo sapiens
US-09-909-320-137
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                                                                             LENGTH: 38
TYPE: PRT
ORGANISM:
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
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                                                                                                                                            Sequence 137, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
                  FSPDOMGRSKESGWVENEIYGY 382
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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                                                                                                                                                                                                             1 MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSR 60
                                                                                                                                                                             1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR 52
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                                                                                                                                   Сарв
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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8
                                                                                          Length 382;
                                                                                                                                 Indels
                                                                                     Ouery Match 99.3%; Score 1986; DB 10; Best Local Similarity 97.9%; Pred. No. 2.7e-178; Matches 374; Conservative 0; Mismatches 0;
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Publication No. US20020192659A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Genentech, Inc
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-137
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361 PSPDQMGRSKESGWVENEIYGY 382

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,824

PRIOR PAPLICATION NUMBER: 2001-07-17

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-01-6

PRIOR PELING DATE: 1999-09-01-6

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-11-00

PRIOR PELING DATE: 1
                                                                                                                                                                           Sequence 137, Application US/09907824 Publication No. US20020197671A1 GENERAL INFORMATION:
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Grimaldi, Christopher
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Pred. No. 2.7e-178;
0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 2000-0105
PRIOR PILING DATE: 2000-0105
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
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Best Local Similarity 97.9
Matches 374; Conservative
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US-09-902-853-137
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61 RINFEBAKBACRRDGGQLVSIESEDBQXLIEKFIENLLPSDGDFWIGLRRREEKGSNSTA 120
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NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.3%; Score 1986; DB 10; Best Local Similarity 97.9%; Pred. No. 2.7e-178; Matches 374; Conservative 0; Mismatches 0;
                  FILE KEKEKKELS: 10490-14

CURRENT PEDLICATION NUMBER: US/09/907,841

CURRENT PILING DATE: 2001-11-20

PRIOR PELING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20544

PRIOR APPLICATION NUMBER: PCT/US99/20544

PRIOR APPLICATION NUMBER: PCT/US99/20544

PRIOR FILING DATE: 1999-09-15

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Publication No. US20030003530A1;
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.;
APPLICANT: Botstein, David;
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-907-841-137
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APPLICANT: BOSTCEAL, AV1

APPLICANT: BOSTCEAL, David

APPLICANT: BECON, Dan L.

APPLICANT: Farcar, Napoleone

APPLICANT: Fond, Sherman

APPLICANT: Fond, Sherman

APPLICANT: Gerriteen, Mary E.

APPLICANT: Gerriteen, Mary E.

APPLICANT: Gerriteen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Goddard, Austin L.

APPLICANT: Goddard, Austin L.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: William, I.

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Desnoyers, Luc
APPLICANT: Besnoyers, Luc
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
                                                                                                         ; ORGANISM: Homo Sapien
US-09-907-824-137
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US-09-907-841-137
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                              1 MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKV1YFHDTSR 60
    52
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    1 MRPGTALQAVLLAVLLVGLRAATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSR
                                                                                         RLNFBEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTA
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-18
APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
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US-09-906-742-137
Sequence 137, Application US/09906742
Fublication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Iuc
APPLICANT: Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION WINBER: US/09/94,011
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 1000-02-20/145,698
PRIOR PLILING DATE: 1000-02-20/145,698
PRIOR PLILING DATE: 1099-07-36
PRIOR PLILING DATE: 1099-07-36
PRIOR PLILING DATE: 1099-03-18
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Pred. No. 2.7e-178;
0; Mismatches 0; Indels 8
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Grimaldi, Christopher J.
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Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
                       Ferrara, Napoleone
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Gerritsen, Mary E.
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Best Local Similarity 97.9%;
Matches 374; Conservative
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                                            Filvaroff, Ellen
                                                                    Fong, Sherman
Gao, Wei-Qiang
Eaton, Dan L.
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) ORGANISM: Homo Sapien
US-09-904-011-137
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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CURRENT PILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-00-22
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/2099
PRIOR PILING DATE: 1999-12-02
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Mather, Jennie P.
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Desnoyers, Luc
Eaton, Dan L.
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ORGANISM:
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PRIOR PILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-8
PRIOR FILING DATE: 1999-08-08
PRIOR PLING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/20944
PRIOR PELING DATE: 1999-09-13
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; ORGANISM: Homo Sapien
US-09-906-742-137
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LENGTH: 382
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99.3%; Score 1986; DB 11; Length 382;

; ORGANISM: Homo Sapien US-09-906-838-137

ઠ g Query Match

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61 RINFEBAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKGSNSTA 120
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Best Local Similarity 97.9%; Pred. No. 2.7e-178;
Matches 374; Conservative 0; Mismatches 0;
                                                                                                                                                                                           PRIOR PILING DATE: 1999-09-15
PRIOR PLILNG DATE: 1999-09-15
PRIOR PLILNG DATE: 1999-09-15
PRIOR PLILNG DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLILNG DATE: 1999-11-29
PRIOR PLILNG DATE: 1999-11-29
PRIOR PLILNG DATE: 1999-11-30
PRIOR PLILNG DATE: 1999-11-30
PRIOR PLILNG DATE: 1999-12-02
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PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 2000-01-05
NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
                              PILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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Publication No. US20030027146A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-907-613-137
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                                                                                                                                                                                                                                                                                                                                                              121 CQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 NFICKYSDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPS 240
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Best Local Similarity 97.9%; Pred. No. 2.7e-178; Matches 374; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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o. US20030027145A1
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Grimaldi, Christopher J.
Gurney, Austin L.
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Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bettein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Publication No. US2
GENERAL INFORMATION
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APPLICANT: Stewart, Intochy A-
APPLICANT: Stewart, Intochy A-
APPLICANT: Williams, Daniel
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
CURRENT APPLICATION WINBER: US/09/907,942
CURRENT APPLICATION WINBER: US/00/04414
PRIOR PELING DATE: 3000-02-22
PRIOR PELING DATE: 3000-02-22
PRIOR PELING DATE: 1999-07-38
PRIOR PELING DATE: 1999-07-38
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Filvaroff, Ellen
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Mather, Jennie P.
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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; ORGANISM: HOI
US-09-907-942-13
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Score 1986; DB 11; Length 382; Pred. No. 2.7e-178;

99.3%;

Query Match Best Local Similarity

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112
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AND THE CHOUNDOITH SULFATE (CS) ATTACHMENT DOWALNS LIE BETWEEN GZ
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CHAINS, NITHER THE CONTAINS WILLY CHOUNDOITH SULFATE BUT ALSO SERAINS SULFATE
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66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVC 121
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